



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 182414

TO: Sheela Huff
Location: rem/3A15/3C18
Art Unit: 1643
Friday, March 17, 2006
Case Serial Number: 10/609217

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518


barbara.obryen@uspto.gov

Search Notes

RUSH

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STIC-Biotech/ChemLib

182414

Mj

From: Huff, Sheela
Sent: Tuesday, February 21, 2006 6:44 AM
To: STIC-Biotech/ChemLib
Subject: search request for 10/609217

Please search and interference search SEQ ID NO. 2.

thanks-

Sheela Huff
Art Unit 1643
571-272-0834
Remsen 3A15
mailbox Remsen 3C18

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIS: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 16, 2006, 19:57:23 ; Search time 191 Seconds
(without alignments)
524.494 Million cell updates/sec

Title: US-10-609-217-2
Perfect score: 1238
Sequence: 1 MDKHTHCPPCPAELLGPPS.....MHEALHNHYQKSLSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Searched:      2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
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A_Geneseq_21*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1238	100.0	228	3	AAE96529	AAE96529 Human IGC
2	1238	100.0	228	3	AAE16955	AAE16955 Human IGC
3	1238	100.0	228	4	AAE98953	AAE98953 Human IGC
4	1238	100.0	228	5	AAE04279	AAE04279 Human IGC
5	1238	100.0	228	5	AAE81074	AAE81074 Human IGC
6	1238	100.0	228	5	AAE14310	AAE14310 Human IGC
7	1238	100.0	228	5	AAE73410	AAE73410 Human IGC
8	1238	100.0	228	5	AAE66012	AAE66012 Human IGC
9	1238	100.0	228	5	AAE73018	AAE73018 Human IGC
10	1238	100.0	228	6	AAE38267	AAE38267 Human IGC
11	1238	100.0	228	7	AAE58683	AAE58683 Human IGC
12	1238	100.0	228	8	AAE11708	AAE11708 Human IGC
13	1238	100.0	228	8	AAE075329	AAE075329 Human IGC
14	1238	100.0	243	3	AAE11957	AAE11957 Human IGC
15	1238	100.0	243	5	AAE87425	AAE87425 Human IGC
16	1238	100.0	243	7	AAE59746	AAE59746 Human IGC
17	1238	100.0	247	3	AAE16958	AAE16958 Human IGC
18	1238	100.0	247	5	AAE73411	AAE73411 Human IGC
19	1238	100.0	248	3	AAE11951	AAE11951 Human IGC
20	1238	100.0	248	3	AAE11953	AAE11953 Human IGC
21	1238	100.0	248	5	AAE73421	AAE73421 Human IGC
22	1238	100.0	248	5	AAE87419	AAE87419 Human IGC
23	1238	100.0	250	7	AAE31616	AAE31616 Human IGC
24	1238	100.0	250	8	AAE11978	AAE11978 Human IGC

25	1238	100.0	252	3	AA817955	Abb17955	PC-VEGF	a
26	1238	100.0	252	5	AB873423	Abb17423	PC-VEGF	a
27	1238	100.0	253	3	AA816964	Abb16964	PC-EMP	Dr
28	1238	100.0	253	5	AB873415	Abb17415	PC-EPO	mi
29	1238	100.0	259	9	AA818572	Abb18572	Hea15572	hmo
30	1238	100.0	268	5	AA816959	Abb16959	PC-TMP-TM	
31	1238	100.0	268	5	AB873412	Abb17412	PC-TMP-TM	
32	1238	100.0	269	3	AA966531	Abb96531	Human IG6	
33	1238	100.0	277	3	AA816967	Abb16967	PC-EMP-EMV	
34	1238	100.0	277	5	AB873418	Abb17418	PC-EMP-EMV	
35	1238	100.0	282	5	AA818169	Abb18169	Echi18169	Echi18169
36	1238	100.0	374	2	AA849075	Abb49075	Recombina	
37	1238	100.0	374	2	AA883963	Abb83963	Recombina	
38	1238	100.0	374	9	AA851285	Abb51285	Recombina	
39	1238	100.0	401	4	AA880504	Abb80504	Human met	
40	1238	100.0	401	4	AA872922	Abb72922	Human met	
41	1235	99.8	406	7	AD875162	Adp75162	Fusion co	
42	1235	99.8	409	7	AD875170	Adp75170	Fusion co	
43	1235	99.8	409	7	AD875176	Adp75176	Fusion co	
44	1235	99.8	410	7	AD875166	Adp75166	Fusion co	
45	1235	99.8	412	7	AD875168	Adp75168	Fusion co	

ALIGNMENTS

RESULT 1
 ID AAY96529
 AAY96529 standard; protein; 228 AA.
 AC AAY96529;
 XX
 DT 04-SEP-2000 (first entry)
 DE
 Human IgG1 Fc chain.
 XX
 KM Immunoglobulin; IgG1; Fc; thrombopoietin; mimetic; TMP; TPO; platelet;
 KM megakaryocyte; production; anti-human immunodeficiency virus; anti-HIV;
 KM anti-anaemic; dermatologically; immunosuppressive; anti-inflammatory.
 XX
 OS Homo sapiens.
 XX
 PN WO200024770-A2.
 PD
 PD 04-MAY-2000.
 PF 22-OCT-1999; 99WO-US024834.
 PR 23-OCT-1998; 98US-0105348P.
 PA (AMGE-) AMGEN INC.
 PI Liu C, Feige U, Cheetham J;
 DR MPI: 2000-365108/31.
 DR N-PSDB; AAA29220.
 PT Thrombopoietic peptides which activate mpl receptors and increase the
 PT production of platelets or platelet precursors, useful for treatment of
 PT diseases which involve thrombocytopenia.
 XX
 PS Disclosure; Page 76-77; 91pp; English.
 CC A compound which binds to an mpl receptor comprising a thrombopoietin
 CC mimetic peptide (TMP) dimer joined by a linker (TMP-1-(L1)-nTMP-2), is
 CC new. TMP-1 and TMP-2 are amino acid sequences varying from at least 10 to
 CC 14 residues in length comprising X-2-X1-0, X-2-X1-1, X-2-X1-2, X-2-
 CC X1-3, X-2-X1-4, X-1-X1-0, X-1-X1-1, X-1-X1-2, X-1-X1-3, and X-1-
 CC X1-4. X1=-I, A, V, L, -S or R; X2=B, D, K or V; X3=G or A; X4=
 CC P, X5=T or S; X6=L, I, V, A or F; X7=R or K; X8=O, N, or E;
 CC X9=W, Y or F; X10=L, I, V, A, F, M, or K; X11=A, I, V, L, P,
 CC S, T, K, H, or E; X12=A, I, V, L, F, G, S, or Q; X13=R, K, T, V,
 CC N, Q or G; X14=A, I, V, L, F, T, R, E, or G; L1=linker comprising

CC 1 to 20 amino acids; and n = 0 or 1. The compounds bind to and activate
 CC the c-Mpl receptor which mediates the activity of endogenous
 CC thrombopoietin. The TmPs are useful for increasing the production of
 CC platelets or platelet precursors (e.g. megakaryocytes) in a mammal, which
 CC is useful for treatment of diseases which involve thrombocytopenia, e.g.
 CC aplastic anaemia, immune thrombocytopenia (ITP), human immunodeficiency
 CC virus associated ITP, and systemic lupus erythematosus
 XX

SO Sequence 228 AA;
 Query Match 100.0%; Score 1238; DB 3; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4,6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPAPLGGPSVFLFPKPKDTLMSRPEVTGVVVDVSHEDPEKFNWYV 60
 DB 1 MDKTHTCPCPAPAPLGGPSVFLFPKPKDTLMSRPEVTGVVVDVSHEDPEKFNWYV 60
 QY 61 DGEVHNNAKTRREQYNSTTRVSVLTVLHQMNLNGEKYCKVSNKALPAPIKETSKA 120
 DB 61 DGEVHNNAKTRREQYNSTTRVSVLTVLHQMNLNGEKYCKVSNKALPAPIKETSKA 120
 QY 121 KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMEHALNHNHYOKSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMEHALNHNHYOKSLSPGK 228

RESULT 2
 AAB16955
 ID AAB16955 standard; protein; 228 AA.

XX AAB16955;

XX 31-OCT-2000 (first entry)

DE Human IgG1 Fc protein sequence SEQ ID NO:2.

XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KW autoimmune disease; cytostatic; antilastmatic; thrombolytic; VEGF;
 KW immunosuppressive; BPO; TPO; CTLA4; mistic; IL-1; TNF; antagonist; MMP;
 KW inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KW cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KW vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KW thrombosis; pharmaceutical.

XX Homo sapiens.

XX WO200024782-A2.

XX 04-MAY-2000.

XX 25-OCT-1999; 99WO-US025044.

XX 23-OCT-1998; 98US-0105371P.

XX 22-OCT-1999; 99US-00428082.

XX (AMGE-) AMGEN INC.

XX Feige U, Liu C, Cheetham J, Boone TC;

XX WPI; 2000-350702/30.

XX N-PSDB; AAA69443.

XX Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX Claim 7; Page 176-177; 608PP; English.

XX The present invention describes composition of matter (I) comprising an

CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)-a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)-C-P1, -(L1)-C-P1-(L2)-d-P2, -(L1)-C-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-C-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antilastmatic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 3; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4,6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPAPLGGPSVFLFPKPKDTLMSRPEVTGVVVDVSHEDPEKFNWYV 60
 DB 1 MDKTHTCPCPAPAPLGGPSVFLFPKPKDTLMSRPEVTGVVVDVSHEDPEKFNWYV 60
 QY 61 DGEVHNNAKTRREQYNSTTRVSVLTVLHQMNLNGEKYCKVSNKALPAPIKETSKA 120
 DB 61 DGEVHNNAKTRREQYNSTTRVSVLTVLHQMNLNGEKYCKVSNKALPAPIKETSKA 120
 QY 121 KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAVWESNGQPENNYKTTTPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMEHALNHNHYOKSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMEHALNHNHYOKSLSPGK 228

RESULT 3
 AAB98953
 ID AAB98953 standard; protein; 228 AA.

XX AAB98953;

XX 14-AUG-2001 (first entry)

DE Human IgG1 Fc region.

XX Human; IgG1; immunoglobulin; Fc region; Fc fusion protein; misfolding;
 KW therapy; cancer; osteoarthritis; AIDS; obesity; inflammation;
 KW transplant rejection.

XX Homo sapiens.

XX WO200134638-A1.

XX 17-MAY-2001.

XX 10-NOV-2000; 2000WO-US030798.

XX 12-NOV-1999; 99US-0165188P.

XX 09-NOV-2000; 2000US-00709704.

XX (AMGE-) AMGEN INC.

XX Treuhelt MJ, O'connor SR, Kosky AA;

XX WPI; 2001-335908/35.

XX N-PSDB; AAH25762.

PT Correcting disulfide bond misfolds in Fc-containing proteins,
 PT particularly therapeutic Fc-containing fusion proteins or antibodies, by
 PT treatment with copper halide.
 XX Claim 30; Fig 5; 59pp; English.
 CC The present invention describes a process for preparing a
 CC pharmacologically active compound, involving preparing a
 CC comprising an immunoglobulin Fc domain fused to a protein of interest,
 CC treating the compound with a copper(II) halide and isolating the treated
 CC molecule. This can be used to correct misfolding of Fc domain containing
 CC proteins, for use in therapeutic agents which may be used in the
 CC treatment of cancer, inflammation, transplant rejection, AIDS,
 CC osteoarthritis and obesity. The present sequence is the IgG1 Fc domain
 XX Sequence 228 AA;
 SQ
 Query Match 100.0%; Score 1238; DB 4; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4,6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDKHTCPCPAPBELLGSPSVFLPPPKKDTLMISRPEVTCVVVDVSHEDPEVKFMYV 60
 DB 1 MDKHTCPCPAPBELLGSPSVFLPPPKKDTLMISRPEVTCVVVDVSHEDPEVKFMYV 60
 QY 61 DGVVHNAKTKRPEEQYNSTYRVVSVLTVLDHQMNLNKEVKKCSNKAALPAPIEKTISKA 120
 DB 61 DGVVHNAKTKRPEEQYNSTYRVVSVLTVLDHQMNLNKEVKKCSNKAALPAPIEKTISKA 120
 QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYTQKSLSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYTQKSLSLSPGK 228
 RESULT 4
 ABB04279 ID ABB04279 standard; protein; 228 AA.
 XX AC ABB04279;
 XX DT 13-FEB-2002 (first entry)
 XX DE Human IgG1 Fc domain.
 XX KM Glucagon antagonist; antidiabetic; anti-hormonal; Fc domain;
 XX KM non-insulin dependent diabetes mellitus; human; immunoglobulin G; IgG.
 XX OS Homo sapiens.
 XX PN WO200183527-A2.
 XX PD 08-NOV-2001.
 XX PF 03-MAY-2001; 2001WO-US014321.
 XX PR 03-MAY-2000; 2000US-0201436P.
 XX PR 02-MAY-2001; 2001US-00847249.
 XX PA (AMGE-) AMGEN INC.
 XX PI Marshall WS, Stark KL;
 XX DR WPI; 2002-017738/02.
 XX DR N-PSDB; ABA03672.
 XX PT Compositions comprising glucagon antagonist domains, useful for treating
 XX PT diabetes mellitus.
 XX PS Claim 8; Fig 2; 54pp; English.

XX The invention relates to compositions comprising a glucagon antagonist
 CC domain and a vehicle, such as a polymer (e.g. PEG or dextran) or,
 CC preferably, an Fc domain. The vehicle is covalently attached to the
 CC glucagon antagonist domain. The compositions are administered to treat
 CC non-insulin dependent diabetes mellitus. The present sequence is the
 CC human IgG Fc domain, which may be used as the vehicle in the compositions
 CC of the invention
 XX Sequence 228 AA;
 SQ
 Query Match 100.0%; Score 1238; DB 5; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4,6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDKHTCPCPAPBELLGSPSVFLPPPKKDTLMISRPEVTCVVVDVSHEDPEVKFMYV 60
 DB 1 MDKHTCPCPAPBELLGSPSVFLPPPKKDTLMISRPEVTCVVVDVSHEDPEVKFMYV 60
 QY 61 DGVVHNAKTKRPEEQYNSTYRVVSVLTVLDHQMNLNKEVKKCSNKAALPAPIEKTISKA 120
 DB 61 DGVVHNAKTKRPEEQYNSTYRVVSVLTVLDHQMNLNKEVKKCSNKAALPAPIEKTISKA 120
 QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYTQKSLSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQQGNVFCSVMEALHNHYTQKSLSLSPGK 228
 RESULT 5
 AAU81074 ID AAU81074 standard; protein; 228 AA.
 XX AC AAU81074;
 XX DT 09-APR-2002 (first entry)
 XX DE Human IgG1 Fc.
 XX KM Human; IgG Fc; anticoagulant; thrombolytic; cytostatic; antiinflammatory;
 XX KM immunosuppressive; osteoprotic; antagonist; laminin; saw-scaled viper;
 XX KM echistatin; integrin; selectin; vinculin; platelet aggregation;
 XX KM angiogenesis; tumour; inflammation; autoimmune disease;
 XX KM rheumatoid arthritis; osteoporosis.
 XX OS Homo sapiens.
 XX PN WO200181377-A2.
 XX PD 01-NOV-2001.
 XX PF 23-APR-2001; 2001WO-US013069.
 XX PR 21-APR-2000; 2000US-0198919P.
 XX PR 03-MAY-2000; 2000US-0201394P.
 XX PA (AMGE-) AMGEN INC.
 XX PI Feige U, Kohno T, Lacey DL, Boone TC;
 XX DR WPI; 2002-062025/08.
 XX DR N-PSDB; ABK24097.
 XX PT Composition comprising integrin or adhesion antagonistic peptide and
 XX PT vehicle, useful for treating or preventing platelet aggregation, has a
 XX PT longer half-life than free peptide.
 XX PS Claim 9; Fig 3; 68pp; English.
 XX The invention relates to a composition comprising an integrin/adhesion

CC antagonistic peptide (1) and a vehicle e.g. IgG Fc. The peptides are
 CC based on laminin or saw-scaled viper echistatin and target integrin,
 CC selectin or vinculin. Also included are compounds of formula (Ia) and X² =
 CC their multimers (X¹) a-F¹-(X²)_b where: F¹ = Fc domain; X¹ and X² =
 CC -(U¹)₁-C-P¹-(U²)₂-d-P², (U¹)₁-C-P¹-(U²)₂-d-P²-(U³)₃-e-
 CC P³ or (U¹)₁-C-P¹-(U²)₂-d-P²-(U³)₃-e-P³-U⁴; F¹-P⁴ = same or
 CC different (1); U¹-U⁴ = same or different linker; a-f = 0 or 1,
 CC provided at least one of a and b = 1, a nucleic acid that encodes (Ia),
 CC an expression vector containing the nucleic acid, host cells containing
 CC the vector, producing a pharmaceutically active compound (B) by
 CC covalently linking at least one Fc domain to at least one amino acid
 CC sequence of a selected randomized (1) and any of six laminin-related
 CC peptides (Ib). The compositions are used prophylactically and
 CC therapeutically in the same way as (1), e.g. to inhibit platelet
 CC aggregation or angiogenesis (tumours), or to treat inflammation and
 CC autoimmune diseases (e.g. rheumatoid arthritis) and many different forms
 CC of osteoporosis, also for diagnosis. Attaching the vehicle (especially Fc
 CC domain) to (1) increases the half-life (free (1) are normally degraded
 CC very quickly in vivo). The present sequence is human IgG1 Fc which is
 CC used as a vehicle for the antagonists of the invention

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKHTGCPAPRLGGPSVFLPPPKDITMISRPETVCVVDVSHEDPEVKFMYV 60
 DB 1 MDKHTGCPAPRLGGPSVFLPPPKDITMISRPETVCVVDVSHEDPEVKFMYV 60
 QY 61 DGEVHNNAKTRREQYNSTYRVSVLTVLHODWLNGEKYCKVSNKALPAPIKITSKA 120
 DB 61 DGEVHNNAKTRREQYNSTYRVSVLTVLHODWLNGEKYCKVSNKALPAPIKITSKA 120
 QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLD 180
 QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLD 180
 QY 181 SDGSFPLYSKLTVDKSRMVGQGVFNFCGVMEHALHNHYTQKSLSLSPGK 228
 DB 181 SDGSFPLYSKLTVDKSRMVGQGVFNFCGVMEHALHNHYTQKSLSLSPGK 228

RESULT 6

AAE14310 ID AAE14310 standard; protein; 228 AA.

XX AAE14310;
 AC 07-MAR-2002 (first entry)
 DT 07-MAR-2002 (first entry)
 XX Human immunoglobulin G (IgG1) Fc.
 DE Human immunoglobulin G (IgG1) Fc.
 XX Human, calcitonin; CT; CT receptor; Fc domain; therapy; osteoporosis;
 KW immunoglobulin G; IgG; osteopathic.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200183526-A2.
 PN 08-NOV-2001.
 PD 08-NOV-2001; 2001WO-US014320.
 XX 03-MAY-2000; 2000US-0201511P.
 PR 02-MAY-2001; 2001US-00847712.
 XX (AMGE-) AMGEN INC.
 PA Liu C, Marshall WS, Reynolds A;
 PI WPI, 2002-034503/04.
 XX DR

DR N-PSDB; AAD23840.
 XX Compositions comprising Calcitonin receptor modulator domains, useful for
 PT treating osteoporosis.

PS Claim 8; Fig 3; 64pp; English.

XX The invention relates to therapeutic agents that modulate the activity of
 CC calcitonin (CT) receptor. Modulators of CT receptor comprise a CT
 CC receptor modulating domain and a vehicle such as a polymer or an Fc
 CC domain, where the vehicle is covalently attached to the CT receptor
 CC modulating domain. The compositions comprising CT receptor modulating
 CC domains are used to treat osteoporosis. The present sequence is human
 CC immunoglobulin G (IgG1) Fc protein used in the invention

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKHTGCPAPRLGGPSVFLPPPKDITMISRPETVCVVDVSHEDPEVKFMYV 60
 DB 1 MDKHTGCPAPRLGGPSVFLPPPKDITMISRPETVCVVDVSHEDPEVKFMYV 60
 QY 61 DGEVHNNAKTRREQYNSTYRVSVLTVLHODWLNGEKYCKVSNKALPAPIKITSKA 120
 DB 61 DGEVHNNAKTRREQYNSTYRVSVLTVLHODWLNGEKYCKVSNKALPAPIKITSKA 120
 QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLD 180
 QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPVLD 180
 QY 181 SDGSFPLYSKLTVDKSRMVGQGVFNFCGVMEHALHNHYTQKSLSLSPGK 228
 DB 181 SDGSFPLYSKLTVDKSRMVGQGVFNFCGVMEHALHNHYTQKSLSLSPGK 228

RESULT 7

ABB73410 ID ABB73410 standard; protein; 228 AA.

XX ABB73410;
 AC 05-APR-2002 (first entry)
 DT 05-APR-2002 (first entry)
 XX Human immunoglobulin G1 Fc (IgG1 Fc) amino acid SEQ ID NO:2.
 DE Human immunoglobulin G1 Fc (IgG1 Fc) amino acid SEQ ID NO:2.
 XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
 KW erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
 KW TNF-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
 KW cyostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antifertility; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative disease; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX Homo sapiens.
 OS Homo sapiens.
 XX WO200183525-A2.
 PN 08-NOV-2001.
 PD 08-NOV-2001; 2001WO-US014310.
 XX 02-MAY-2001; 2001US-00563286.
 PR 03-MAY-2000; 2000US-00563286.
 XX (AMGE-) AMGEN INC.
 PA
 XX DR

PI Feige U, Liu C, Cheecham JC, Boone TC, Gudas JM;
 XX WPI; 2002-130313/17.
 DR N-PSDB; ABL35760.
 XX Novel vehicle-peptide molecule or its multimers useful for treating
 PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
 PT diabetic retinopathy, obesity, sleep disorders and infertility.
 XX
 PS Claim 7; Fig 4; 176pp; English.

XX The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers, (I) can have antiinflammatory, antitumor, immunosuppressive,
 CC cytoskeletal, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC anti-neurotic, anorectic, antifertility, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The EPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKHTCTPCPAPBLTGGPSVFLPPPKDITMTSRPEVTCVVDVSHDEPEKFMVY 60
 DB 1 MDKHTCTPCPAPBLTGGPSVFLPPPKDITMTSRPEVTCVVDVSHDEPEKFMVY 60
 QY 61 DGEVHNAAKTPREBOINSTRVSVTLVTHQDNLNGEKYCKVSNKALPAPIEKTISKA 120
 DB 61 DGEVHNAAKTPREBOINSTRVSVTLVTHQDNLNGEKYCKVSNKALPAPIEKTISKA 120
 QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMHGALHNHTYQKLSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMHGALHNHTYQKLSLSPGK 228

RESULT 8
 ID AAG66012 standard; protein; 228 AA.

XX AAG66012;
 AC AAG66012;
 DT 27-FEB-2002 (first entry)
 XX Human immunoglobulin (Ig) G1 Fc region sequence.
 DB Human immunoglobulin (Ig) G1 Fc region sequence.
 XX Apo-AI, amphipathic; pharmaceutical; peptide mimic; antilipemic;
 KM anti-HIV; virucide; immunoglobulin; IgG1.
 XX Homo sapiens.
 OS
 XX WO200181376-A2.

XX 01-NOV-2001.
 PD
 XX 23-APR-2001; 2001MO-US013068.
 PF
 XX 21-APR-2000; 2000US-0198920P.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX
 XX Kohno T;
 PI
 XX WPI; 2002-049262/06.
 DR N-PSDB; AAI67658.
 XX

PT Recombinant or modified therapeutic agents having Apo-AI amphipathic
 PT helix peptide activity useful in treatment of hypercholesterolemia and
 PT viral infections such as herpes simplex virus, human immunodeficiency
 PT virus.
 XX
 XX Claim 8; Fig 3A-B; 49pp; English.

XX The invention provides a composition comprising a therapeutic agent that
 CC has activity similar to Apo-AI amphipathic helix peptide, but with better
 CC pharmaceutical characteristics attached to a vehicle through the
 CC peptide's N-terminus or C-terminus having a specified formula. The
 CC peptide mimic has greater half-life compared to conventional Apo-AI
 CC amphipathic helix peptide. The compositions are useful for treating
 CC hypercholesterolemia and viral infection such as HIV, HSV. The present
 CC sequence represents the human immunoglobulin (Ig) G1 Fc region which acts
 CC as a vehicle

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKHTCTPCPAPBLTGGPSVFLPPPKDITMTSRPEVTCVVDVSHDEPEKFMVY 60
 DB 1 MDKHTCTPCPAPBLTGGPSVFLPPPKDITMTSRPEVTCVVDVSHDEPEKFMVY 60
 QY 61 DGEVHNAAKTPREBOINSTRVSVTLVTHQDNLNGEKYCKVSNKALPAPIEKTISKA 120
 DB 61 DGEVHNAAKTPREBOINSTRVSVTLVTHQDNLNGEKYCKVSNKALPAPIEKTISKA 120
 QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLD 180
 DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMHGALHNHTYQKLSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMHGALHNHTYQKLSLSPGK 228

RESULT 9
 ID AAU73018 standard; protein; 228 AA.

XX AAU73018;
 AC AAU73018;
 DT 12-MAR-2002 (first entry)
 XX Human immunoglobulin G (IgG) Fc region.
 DB Human immunoglobulin G (IgG) Fc region.
 XX Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KM PTHrP; bone resorption inhibitor; osteoprotegerin; OP; OPG-L antibody;
 KM calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KM osteopontin; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KM breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KM Paget's disease; osteomyelitis; osteonecrosis; bone cell death.
 KM Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KM rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KM immunoglobulin G; IgG.

XX Homo sapiens.
 OS WO200181415-A2.
 PN 01-NOV-2001.
 PD 27-APR-2001; 2001WO-US013528.
 PF 27-APR-2000; 2000US-0200053P.
 PR 28-JUN-2000; 2000US-0214866P.
 PR 06-FEB-2001; 2001US-0266673P.
 PR 26-APR-2001; 2001US-00843221.
 XX (AMGE-) AMGEN INC.
 PA
 XX Koestenuik P, Liu C, Lacey DL;
 PI WPI; 2002-066435/09.
 XX DR N-PSDB; AAS97392.
 DR
 XX Composition, useful for treating osteopenia, comprises parathyroid hormone and parathyroid hormone-related protein receptor modulators.
 PT
 XX Claim 6; Fig 3; 107pp; English.

XX The invention relates to a composition (I) comprising modulators of parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP) which comprise a PTH/PTHrP modulating domain and a vehicle. (I) comprising PTH agonist optionally with a bone resorption inhibitor, such as osteoprotegerin (OPG), OPG-L antibody, calcitonin, bisphosphonates, oestrogen, oestrogen receptor modulators and tibolone is useful for treating osteopenia. (I) is useful for therapeutic and prophylactic purposes. Antagonists of PTH receptor are useful in treating primary and secondary hyperthyroidism, hypercalcaemia, tumour metastases, particularly breast and prostate cancer, cachexia and anorexia, osteopenia, including various forms of osteoporosis, Paget's disease of bone, osteomyelitis, osteonecrosis or bone cell death, associated with traumatic injury or nontraumatic necrosis associated with Gaucher's disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid arthritis, periodontal disease and alopecia. PTH receptor agonists are useful as therapeutic agents in conditions including fracture repair (including healing of non-union fractures), osteopenia, including various forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone and parathyroid hormone related protein (PTH/PTHrP) modulators and related amino acid sequences of the invention

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 5; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYV 60
 DB 1 MDKTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYV 60
 QY DGEVHNNAKTKPREQVNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKKA 120
 DB 61 DGEVHNNAKTKPREQVNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKKA 120
 QY 121 KGQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLD 180
 DB 121 KGQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMEALAHNHYTKSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMEALAHNHYTKSLSPGK 228

RESULT 10
 ABU38267 standard; protein; 228 AA.

XX ABU38267;
 AC 12-JUN-2003 (first entry)
 DT
 XX Human IgG1 Fc protein SEQ ID NO 2.
 DE
 XX

XX TALL-1-binding protein; TALL-1; B-cell-mediated autoimmune disease;
 KW systemic lupus erythematosus; B-cell-mediated cancer; lymphoma;
 KW inflammation; rheumatoid arthritis; acute pancreatitis; atherosclerosis;
 KW Alzheimer's disease; asthma; cachexia; cirrhosis; diabetes; osteoporosis;
 KW glomerulonephritis; Hashimoto's thyroiditis; ischaemic injury; psoriasis;
 KW multiple myeloma; multiple sclerosis; Parkinson's disease; vasculitis;
 KW gene therapy; human IgG1Fc; human.

XX Homo sapiens.
 OS WO200292620-A2.
 PN 21-NOV-2002.
 PD 13-MAY-2002; 2002WO-US015273.
 PF 11-MAY-2001; 2001US-0290196P.
 PR
 XX (AMGE-) AMGEN INC.

XX Min H, Hsu H;
 PI WPI; 2003-156719/15.
 XX DR N-PSDB; AAT33856.

XX New TALL-1-binding polypeptide, useful for modulating the activity of TALL-1 and in treating, preventing or diagnosing a B-cell-mediated autoimmune disease, cancers or lymphomas.

XX Claim 36; Fig 3; 236pp; English.

XX The invention relates to a novel TALL-1-binding polypeptide comprising a defined sequence in the specification. The composition is useful in modulating the activity of TALL-1, and in treating, preventing, ameliorating, diagnosing or prognosing a B-cell-mediated autoimmune disease (e.g. systemic lupus erythematosus) or B-cell-mediated cancer or lymphoma. The composition may also be used in treating inflammations (e.g. rheumatoid arthritis), acute pancreatitis, Alzheimer's disease, asthma, atherosclerosis, cachexia, cirrhosis, diabetes, glomerulonephritis, Hashimoto's thyroiditis, ischaemic injury, multiple myeloma, multiple sclerosis, osteoporosis, Parkinson's disease, psoriasis and vasculitis. Disorders may be treated with the novel composition using gene therapy. This sequence represents a human IgG1Fc protein relating to the TALL-1 sequence of the invention

XX Sequence 228 AA;

Query Match 100.0%; Score 1238; DB 6; Length 228;
 Best Local Similarity 100.0%; Pred. No. 4.6e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYV 60
 DB 1 MDKTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNNYV 60
 QY DGEVHNNAKTKPREQVNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKKA 120
 DB 61 DGEVHNNAKTKPREQVNSTYRVVSVLTVLHQDLNKGKEYCKVSNKALPAPIEKTISKKA 120
 QY 121 KGQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLD 180
 DB 121 KGQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPYPSDIAVWESNGQPENNYKTTTPVLD 180
 QY 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMEALAHNHYTKSLSPGK 228
 DB 181 SDGSFFLYSKLTVDKSRWQGNVSCSVMEALAHNHYTKSLSPGK 228

RESULT 11
ADN59683
ID ADN59683 standard; protein; 228 AA.
XX
AC ADN59683;
XX
DT 01-JUN-2004 (first entry)
XX
DE Human IgG1 Fc amino acid sequence, seq id 32.
XX
KW Haemostatic; antianaemic; immunosuppressive; platelet;
KW transmembrane signaling; mpl receptor; thrombopoietin mimetic peptide;
KW TM; c-mpl receptor; platelet precursor; megakaryocyte;
KW thrombocytopenia; aplastic anaemia; autoimmune thrombocytopenia;
KW autoimmune haemolytic anaemia; Hughes's syndrome;
KW lupoid thrombocytopenia; IgG1.
XX
OS Homo sapiens.
XX
PN MO2003031589-A2.
XX
PD 17-APR-2003.
XX
PF 11-OCT-2002; 2002MO-US032552.
XX
PR 11-OCT-2001; 2001US-0328666P.
XX
PR 10-OCT-2002; 2002US-00269806.
XX
PA (AMGB-) AMGEN INC.
XX
PI Min H, Sitney KC, Hartley C;
XX
XX WPI; 2003-403101/38.
XX
DR N-PSDB; ADN59682.
XX
PT Novel thrombopoietin mimetic peptides which bind to mpl receptor, and
PT which stimulate the production of platelets and/or the production of
PT platelet precursors, useful for treating thrombocytopenia.
XX
PS Disclosure; SEQ ID NO 32; 126bp; English.
XX
CC The invention relates to a thrombopoietin mimetic peptide (TMP) (I) that
CC binds to the c-mpl (mpl) receptor, and which stimulates the production of
CC platelets and/or the production of platelet precursors, is new. Further
CC disclosed is a composition of matter (II) that binds to an mpl receptor,
CC and a pharmaceutical composition comprising (II) and a carrier. The
CC pharmaceutical composition of the invention is useful for treating
CC thrombocytopenia in an animal, and for increasing megakaryocytes or
CC platelets in a patient. The TMP of the invention is useful for treating
CC conditions involving a megakaryocyte and/or platelet deficiency, e.g.
CC disease conditions involving thrombocytopenia such as aplastic anaemia,
CC autoimmune thrombocytopenia, drug induced immune thrombocytopenia,
CC autoimmune hemolytic anaemia, Hughes's syndrome and lupoid
CC thrombocytopenia. The TMP of the invention is also useful for
CC maintaining the viability or storage life of platelets and/or
CC megakaryocytes and its derived cells. The compounds demonstrate an
CC improved ability to bind to and/or trigger transmembrane signal through,
CC i.e. activating, the mpl receptor the compounds have superior
CC thrombopoietic activity, i.e. the ability to stimulate, in vivo and in
CC vitro, the production of platelets and/or megakaryocytopenic activity,
CC i.e. the ability to stimulate, in vivo and in vitro, the production of
CC platelet precursors. Further, certain of the compounds also exhibit
CC superior therapeutic properties, such as improved plasma half-life,
CC biological activity and in vivo circulation time. The current sequence
CC represents the human IgG1 Fc protein that may be used as a preferred
CC vehicle of the invention.
XX
SQ Sequence 228 AA;
Query Match 100.0%; Score 1238; DB 7; Length 228;
Best Local Similarity 100.0%; Pred. No. 4, 6e-90;

Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKHTTCCPCAPAPELLGGPSVFLTPPPKQDTMTSTPEVTGVVVDVSHDPEKEMVY 60
DB 1 MDKHTTCCPCAPAPELLGGPSVFLTPPPKQDTMTSTPEVTGVVVDVSHDPEKEMVY 60
QY 61 DGEVHNAAKTPREEQNSTFRVSVTLVTHQDMLNGEKYCKYSNKALPAPIKTIKSKA 120
DB 61 DGEVHNAAKTPREEQNSTFRVSVTLVTHQDMLNGEKYCKYSNKALPAPIKTIKSKA 120
QY 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPLD 180
DB 121 KGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPPLD 180
QY 181 SDGSFFLYSKLTVDKSRWQQGNVSCGVMHRLAHNTQKSLSLSPK 228
DB 181 SDGSFFLYSKLTVDKSRWQQGNVSCGVMHRLAHNTQKSLSLSPK 228
RESULT 12
ADM17708
ID ADM17708 standard; protein; 228 AA.
XX
AC ADM17708;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human IgG1 Fc protein SEQ ID NO:60.
XX
KW nerve growth factor modulator; NGF modulator; analgesic; NGF inhibitor;
KW nerve growth factor inhibitor; neurologic pain; diabetic neuropathy;
KW post-herpetic neuralgia; inflammatory pain; migraine; asthma;
KW hyperactive bladder; psoriasis; cancer; acute pain; dental pain;
KW surgical pain; pain; causalgia; demyelinating disease;
KW trigeminal neuralgia; chronic alcoholism; stroke; thalamic pain syndrome;
KW diabetes; acquired immuno deficiency syndrome; AIDS; headache;
KW inflammation; arthritis; rheumatic disease; lupus; osteoarthritis;
KW inflammatory bowel disorder; inflammatory eye disorder; sunburn;
KW carditis; dermatitis; myositis; neuritis; collagen vascular disease;
KW chronic inflammatory condition; neuropathic pain; gastrointestinal; wound;
KW burn; allergic skin reaction; pruritus; vitiligo;
KW gastrointestinal disorder; colitis; gastric ulceration; duodenal ulcer;
KW human; IgG1 Fc; immunoglobulin G.
XX
OS Homo sapiens.
XX
PN MO2004026329-A1.
XX
PD 01-APR-2004.
XX
PF 19-SEP-2003; 2003MO-US029866.
XX
PR 19-SEP-2002; 2002US-0412524P.
XX
PR 18-SEP-2003; 2003US-0066480.
XX
PA (AMGB-) AMGEN INC.
XX
PI Boone TC, Wild KD, Sitney KC, Min H, Kimmel B;
XX
XX WPI; 2004-283150/26.
XX
DR N-PSDB; ADM17707.
XX
DT Novel peptide capable of modulating nerve growth factor activity, useful
DT for treating disease or disorder e.g., acute pain, dental pain, cancer,
DT migraine and collagen vascular disease.
XX
XX Claim 16; SEQ ID NO 60; 267bp; English.
XX
CC The present invention describes a peptide (I) that is capable of
CC modulating nerve growth factor (NGF) activity. Also described: (1)
CC modified peptide (II) comprising (I) and a vehicle, where the modified
CC peptide is capable of modulating NGF activity; (2) dimer or multimer of
CC (I); (3) modified peptide (III), its multimers or its salt, where the

peptide is capable of modulating NGF activity; (4) polynucleotide (IV) encoding (I), (II) or (III); (5) expression vector (V) comprising (IV); (6) host cell (VI) comprising (V); (7) a composition (VII) of matter and a vehicle, where the composition of matter is capable of modulating NGF activity; and (8) pharmaceutical composition comprising (I), (II) or (III) and a diluent or carrier. (I) has analgesic activity, and can be used as an inhibitor of NGF. (I) is useful for treating or preventing a disease or disorder associated with NGF activity by administering (I) to human or animal. The disease or disorder chosen from neurologic pain, painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain, painful diabetic neuropathy, post-herpetic neuralgia, inflammatory pain, migraine, asthma, hyperactive bladder, psoriasis, cancer, acute pain, dental pain, pain from trauma, surgical pain, pain resulting from amputation or abscesses, causalgia, demyelinating diseases, trigeminal neuralgia, chronic alcoholism, stroke, thalamic pain syndrome, diabetes, acquired immuno deficiency syndrome (AIDS), toxins and chemotherapy, general headache, cluster headache, mixed-vascular and non-vascular syndromes, tension headache, general inflammation, arthritis, rheumatic diseases, lupus, osteoarthritis, inflammatory bowel disorders, inflammatory eye disorders, inflammatory or unstable bladder disorders, skin complaints with inflammatory components, sunburn, carditis, dermatitis, myositis, neuritis, collagen vascular diseases, chronic inflammatory conditions, inflammatory pain associated hyperalgesia and allodynia, neuropathic pain and associated hyperalgesia and allodynia, diabetic neuropathy pain, sympathetically maintained pain, deafferentation syndromes, epithelial tissue damage or dysfunction, herpes simplex, post-herpetic neuralgia, disturbances of visceral motility at respiratory, genitourinary, gastrointestinal or vascular regions, wounds, burns, allergic skin reactions, pruritus, vitiligo, general gastrointestinal disorders, colitis, gastric ulceration, duodenal ulcers, vasomotor or allergic rhinitis, or bronchial disorders. (I) is also useful for modulating pain or promoting analgesia by administering (I) to human or animal. (I) is also useful in the manufacture of medicament for the treatment of disease or disorder. The present sequence is used in the exemplification of the present invention.

XX Sequence 228 AA:

Query Match 100.0%; Score 1238; DB 8; Length 228;
Best Local Similarity 100.0%; Pred. No. 4,6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMYV 60
DB 1 MDKTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMYV 60
QY 61 DGEVHNAAKTPREEQNSTYRVVSVLTVLHQDLNKGKEYKCKSNKALPAPIETKTSKA 120
DB 61 DGEVHNAAKTPREEQNSTYRVVSVLTVLHQDLNKGKEYKCKSNKALPAPIETKTSKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPYLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPYLD 180
QY 181 SDGSFPLYSKLTVDKSRWQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFPLYSKLTVDKSRWQGNVFSQVMHEALHNHYTQKSLSLSPGK 228

RESULT 13

ADQ75329 ID ADQ75329 standard; protein; 228 AA.

AC ADQ75329;

DT 07-OCT-2004 (first entry)

DE Human IgG1 Fc protein.

KW parathyroid hormone; parathyroid hormone-related protein; PTH; PTHrP; osteopontin; osteopontin; IgG Fc; antibody.

OS Homo sapiens.

XX

PN WO2004060386-A1.
XX 22-JUL-2004.
PD 01-NOV-2002; 2002MO-US036419.
XX 01-NOV-2002; 2002MO-US036419.
PR 01-NOV-2002; 2002MO-US036419.
XX (AMGE-) AMGEN INC.
PA Kostenuik P, Gegg CV, Jarosinski MA, Kinstler OB;
PI WPI; 2004-543796/52.
DR
XX New composition of matter comprising parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP) modulating domain and a vehicle, or its multimers, useful for treating osteopenia.
PT
XX Disclosure; Fig 3A-C; 132pp; English.

The invention relates to a composition comprising the formula (I): (I) P1-(L1)a-F1, where F1 = a vehicle and is attached at the C-terminus of P1-(L1)a or through a sidechain at any residue from residue 14 through the C-terminal residue; P1 = a parathyroid hormone/parathyroid hormone-related protein (PTH/PTHrP) modulating domain; L1 is a linker; and a = 0 or 1. The composition of matter is useful for treating osteopenia. This sequence corresponds to a human IgG Fc used in the invention.

XX Sequence 228 AA:

Query Match 100.0%; Score 1238; DB 8; Length 228;
Best Local Similarity 100.0%; Pred. No. 4,6e-90;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMYV 60
DB 1 MDKTHTCPCPAPBLGGPSVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFMYV 60
QY 61 DGEVHNAAKTPREEQNSTYRVVSVLTVLHQDLNKGKEYKCKSNKALPAPIETKTSKA 120
DB 61 DGEVHNAAKTPREEQNSTYRVVSVLTVLHQDLNKGKEYKCKSNKALPAPIETKTSKA 120
QY 121 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPYLD 180
DB 121 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEMESNGQPENNYKTPPYLD 180
QY 181 SDGSFPLYSKLTVDKSRWQGNVFSQVMHEALHNHYTQKSLSLSPGK 228
DB 181 SDGSFPLYSKLTVDKSRWQGNVFSQVMHEALHNHYTQKSLSLSPGK 228

RESULT 14

AA17957 ID AA17957 standard; protein; 243 AA.

AC AA17957;

DT 31-OCT-2000 (first entry)

DE FC-MMP inhibitor fusion protein sequence SEQ ID NO:1068.

KW Modified peptide; therapeutic agent; fusion; Fc domain; cancer; autoimmune disease; cytostatic; antineoplastic; thrombolytic; VEGF; immunosuppressive; BPO; TPO; CTLA4; mimetic; IL-1; TNF; antagonist; MMP; inhibitor; erythropoietin; thrombopoietin; interleukin 1; cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor; vascular endothelial growth factor; matrix metalloproteinase; asthma; thrombosis; pharmaceutical.

OS Synthetic.

XX WO20024782-A2.

XX

PD 04-MAY-2000.
 XX 25-OCT-1999; 99MO-US025044.
 XX 23-OCT-1998; 98US-0105371P.
 PR 23-OCT-1999; 99US-00428082.
 XX (AMGE-) AMGEN INC.
 PA Feige U, Liu C, Cheatham J, Boone TC,
 XX WPI; 2000-350702/30.
 DR N-PSDB; AAA69507.
 PT Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 PS Example 7, Page 585-586; 608pp; English.
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)-a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from: -(L1)-c-P1, -(L1)-c-P1-(L2)-d-P2, -(L1)-c-P1-
 CC (L2)-d-P2-(L3)-e-P3, or -(L1)-c-P1-(L2)-d-P2-(L3)-e-P3-(L4)-f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antitumoric,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fab domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAA69443 to AAA69526 and AAB16955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 243 AA;
 Query Match 100.0%; Score 1238; DB 3; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDKTHTCPCPAPAPLGGPSVFLFPKPKDTLMISRPEVTGVVVDVSHDEPKFNMVY 60
 DB 1 MDKTHTCPCPAPAPLGGPSVFLFPKPKDTLMISRPEVTGVVVDVSHDEPKFNMVY 60
 QY 61 DGVEVHNAKTKPRBEQYNSTYRVVSVLTVTHQOMLNKEVKCKVSNKALPAPKEKTSKA 120
 DB 61 DGVEVHNAKTKPRBEQYNSTYRVVSVLTVTHQOMLNKEVKCKVSNKALPAPKEKTSKA 120
 QY 121 KGQPREQVYTLTPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 180
 DB 121 KGQPREQVYTLTPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 180
 QY 181 SDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPK 228
 DB 181 SDGSFFFLYSKLTVDKSRWQQGNVSCSVMHEALHNHYTQKSLSLSPK 228
 RESULT 15
 ABB73425 standard; protein; 243 AA.
 XX ABB73425;
 XX 05-APR-2002 (first entry)
 DE Fc-MMP inhibitor fusion nucleic acid SEQ ID NO:1067.
 XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; BPO;
 KM erythropoietin; TPO; tumour necrosis factor alpha inhibitor;

KW TNP-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
 KW TPO mimetic peptide; EPO mimetic peptide; EMP; VEGF antagonist;
 KW MMP inhibitor; antiinflammatory; antitumor; immunosuppressive;
 KW cytostatic; antirheumatic; antiarthritic; antidiabetic; ophthalmological;
 KW antianemic; anorectic; antiinfectivity; haemostatic; dermatological;
 KW neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
 KW cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
 KW sleep disorder; neurological degenerative diseases; anaemia;
 KW thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
 KW Fanconi's syndrome.
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX WO200183525-A2.
 XX
 PD 08-NOV-2001.
 XX
 PF 02-MAY-2001; 2001MO-US014310.
 XX
 PR 03-MAY-2000; 2000US-00563286.
 XX
 PA (AMGE-) AMGEN INC.
 PI Feige U, Liu C, Cheatham JC, Boone TC, Gudas JM;
 XX WPI; 2002-130313/17.
 DR N-PSDB; ABL35775.
 XX
 PS Example 7, Fig 25A-B; 176pp; English.
 XX
 CC The present invention describes a vehicle-peptide molecule (I) or its
 CC multimers. (I) can have antiinflammatory, antitumor, immunosuppressive,
 CC cytostatic, antirheumatic, antiarthritic, antidiabetic, ophthalmological,
 CC antianemic, anorectic, antiinfectivity, haemostatic, dermatological and
 CC neuroprotective activities. (I) can be used as a therapeutic or
 CC prophylactic agent as well as for screening purposes. (I) is useful for
 CC diagnosing diseases characterised by dysfunction of their associated
 CC protein of interest, for identifying normal or abnormal proteins of
 CC interest, as a part of diagnostic kit to detect the presence of their
 CC proteins of interest in a biological sample. Additionally, (I) is useful
 CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
 CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
 CC infertility, and neurological degenerative diseases. (I), comprising EPO-
 CC mimetic compounds are useful for treating disorders characterised by low
 CC red blood cell levels such as anaemia. The TPO-mimetic comprising
 CC compounds are useful for treating conditions that involve an existing
 CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
 CC deficiency, such as thrombocytopaenia, aplastic anaemia, metastatic
 CC tumour which result in thrombocytopaenia, systemic lupus erythematosus,
 CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
 CC represent amino acid and nucleic acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 243 AA;
 Query Match 100.0%; Score 1238; DB 5; Length 243;
 Best Local Similarity 100.0%; Pred. No. 5e-90;
 Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDKTHTCPCPAPAPLGGPSVFLFPKPKDTLMISRPEVTGVVVDVSHDEPKFNMVY 60
 DB 1 MDKTHTCPCPAPAPLGGPSVFLFPKPKDTLMISRPEVTGVVVDVSHDEPKFNMVY 60
 QY 61 DGVEVHNAKTKPRBEQYNSTYRVVSVLTVTHQOMLNKEVKCKVSNKALPAPKEKTSKA 120
 DB 61 DGVEVHNAKTKPRBEQYNSTYRVVSVLTVTHQOMLNKEVKCKVSNKALPAPKEKTSKA 120
 QY 121 KGQPREQVYTLTPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 180

Db	121	KGQPRBPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVYLD	180
Qy	181	SDGSFPLYSKLTVDKSRWQGQGNVFCSCVMHEALHNHYTQKSLSLSPGK	228
Db	181	SDGSFPLYSKLTVDKSRWQGQGNVFCSCVMHEALHNHYTQKSLSLSPGK	228

Search completed: March 16, 2006, 20:04:37
 Job time : 194 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 16, 2006, 20:01:37 ; Search time 40 Seconds

(without alignments)
548.436 Million cell updates/sec

Title: US-10-609-217-2

Perfect score: 1238
Sequence: 1 MDKHTCPCPAPAPRLGSPS.....MHEALNHHTYQKSLSPGK 228

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*

1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	99.6	255	4	S31866
2	1233	99.6	330	1	GHRU
3	1227	99.1	374	2	S69339
4	1180	95.3	234	2	PT0207
5	1146	92.6	377	2	A23511
6	1144	92.4	377	2	A60764
7	1142.5	92.3	326	1	G2HU
8	1135	91.7	327	1	G2HU
9	1121	90.5	289	1	G3HWT1
10	918.5	74.2	323	1	GHRB
11	906.5	73.2	328	2	I47160
12	906.5	73.0	328	2	I47159
13	903.5	73.0	277	2	I47162
14	889	71.8	329	1	G2GP
15	885.5	71.5	328	2	I47158
16	878.5	71.0	328	2	I47161
17	855.5	69.1	470	2	S22080
18	846	68.3	308	2	G30554
19	846	68.3	472	2	S31459
20	845.5	68.3	329	1	G3MSC
21	838	67.7	333	2	PS0018
22	834.5	67.4	398	1	G3MSM
23	827.5	66.8	444	2	PC4436
24	818.5	66.1	326	2	PS0017
25	817.5	66.0	324	1	G3MS
26	812.5	65.6	329	1	G3MSM
27	809.5	65.4	329	1	S00847
28	809	65.3	330	1	G3MSA
29	809	65.3	469	2	S37483

30	804	64.9	399	1	G2MSAM	Ig gamma-2a chain
31	802	64.8	335	1	G2MSAB	Ig gamma-2a chain
32	794	64.1	446	2	S40295	Ig gamma-2a chain
33	785.5	63.4	322	2	PS0019	Ig gamma-2a chain
34	779	62.9	474	1	G2MS11	Ig gamma-2b chain
35	774	62.5	405	1	G2MS1M	Ig gamma-2b chain
36	764	61.7	327	2	S06611	Ig gamma-2b chain
37	757	61.1	475	2	S01331	Ig gamma-2b chain
38	707	57.1	180	2	I46732	Ig gamma heavy chain
39	577.5	46.6	249	2	S69340	Ig heavy chain VHI
40	574.5	46.4	218	2	A36040	Ig heavy chain V-I
41	571	46.1	41	1	S14236	Ig gamma-1 chain C
42	395.5	31.9	572	2	B46529	Ig y heavy chain (
43	358	28.9	343	2	S25644	Ig mu chain C regi
44	358	28.9	453	2	S37768	Ig mu chain C regi
45	357.5	28.9	549	2	S04845	Ig heavy chain pre

ALIGNMENTS

```

RESULT 1
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
R:Filipula, D.
submitted to the EMBL Data Library, February 1993
A:Description: Screening method for protein-protein interactions of cloned gene products.
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <Full>
A:Cross-references: UNIPARC:UPI000011P41F; EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID
C:Keywords: immunoglobulin
F:1-32/region: Escherichia coli outer membrane protein A precursor
F:23-255/region: human Ig gamma-1 chain C region

Query Match          99.6%; Score 1233; DB 4; Length 255;
Best Local Similarity 100.0%; Pred. No. 5.7e-89;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTTCCPPAPAPRLGSPSVFLPPPKDXTLMISRTBEVTCVVVDVSHEDPEVKFNMYVD 61
DB 29 DKHTTCCPPAPAPRLGSPSVFLPPPKDXTLMISRTBEVTCVVVDVSHEDPEVKFNMYVD 88
QY 62 GVEVHNAKTKPREEQVSTYRVVSVLTVLHQDWLNGKEYCKVKNKALPAPIEKTISKAK 121
DB 89 GVEVHNAKTKPREEQVSTYRVVSVLTVLHQDWLNGKEYCKVKNKALPAPIEKTISKAK 148
QY 122 GQPREPQVYTLPPSRDELTLKNQVSLTCLVKGFSYSDIAVEMESNGQENNYKTPPVLD 181
DB 149 GQPREPQVYTLPPSRDELTLKNQVSLTCLVKGFSYSDIAVEMESNGQENNYKTPPVLD 208
QY 182 DGSFPLYSKLTVDKSRWQQGNVSPCSVMHEALNHHTYQKSLSPGK 228
DB 209 DGSFPLYSKLTVDKSRWQQGNVSPCSVMHEALNHHTYQKSLSPGK 255

RESULT 2
GHRU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence_revision 18-Aug-1982 #text_change 09-Jul-2004
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91223; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.B.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238; PMID:6287432
A:Accession: A93433
A:Molecule type: DNA

```


A:Residues: 1-330 <BL>
A:Cross-references: UNIPROT:P01857; UNIPARC:UPI0000034C0E; EMBL:Z17370
A:Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers,
A:Note: Lys-330 is removed after translation
R:Harrie, U.J.
submitted to the EMBL Data Library, October 1992
A:Accession: S33861
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: UNIPARC:UPI000013C6FE; EMBL:Z17370
R:Ikahashi, N.; Ueda, S.; Odate, M.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943; PMID:6811139
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113;235-330 <TAK>
A:Cross-references: UNIPARC:UPI000017378B; UNIPARC:UPI000017378C; EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammag-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024; PMID:5489771
A:Contents: myeloma protein Bu
A:Accession: B90563
A:Molecule type: protein
A:Residues: 1-96,'R','98-135 <CUN>
A:Cross-references: UNIPARC:UPI000017378D
A:Note: this sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammag-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025; PMID:5530842
A:Contents: Bu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154,'Q','156-165,'Q','167-176,'Q','178-194,'N','196-197,'D','199-238,'E',240,
A:Cross-references: UNIPARC:UPI000017378E
A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Postnig, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nile),
Igen Primerstruktur.
A:Reference number: A91668; MUID:77070269; PMID:826475
A:Contents: myeloma protein Nile
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34,'Q','36-96,'K','98-115,'Q','117-197,'D','199-238,'D',240,'L',242-268,'E',27
A:Cross-references: UNIPARC:UPI000017378F
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289311; PMID:6884994
A:Contents: myeloma protein KOI; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96,'R','98-197,'D','199-238,'B',240,'W',242-266,'D',268-271,'D',273-330 <SCH
A:Cross-references: UNIPARC:UPI0000173790
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammag-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027; PMID:4923144
A:Contents: annotation; disulfide bonds
R:Decker, L.; Schwarz, U.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbomic cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267; PMID:1002129
A:Contents: annotation; disulfide bonds
C:Gene: GDB:IGHG1

A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1; 114/1; 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:137-206/Domain: immunoglobulin homology <IM2>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #stratus experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 99.6%; Score 1233; DB 1; Length 330;

Best Local Similarity 100.0%; Pred. No. 7, 9e-89;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DKHTCPPCPAPELLGSPVFLFPPKXDTLMSRTPEVTCVVVDVSHEDPEVKFNYYVD 61
Db 104 DKHTCPPCPAPELLGSPVFLFPPKXDTLMSRTPEVTCVVVDVSHEDPEVKFNYYVD 163
Qy 62 GVEVHNAKTKRREQNSTRVSVLTFLVDWNGKEYCKVSNKALPAPIETISKAK 121
Db 164 GVEVHNAKTKRREQNSTRVSVLTFLVDWNGKEYCKVSNKALPAPIETISKAK 223
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLD 181
Db 224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTPPVLD 283
Qy 182 DGSFPLSKLTVDKSRWQQGNVSCVMEHALLHNYTKSLSPGK 228
Db 284 DGSFPLSKLTVDKSRWQQGNVSCVMEHALLHNYTKSLSPGK 330

RESULT 3

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C:date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000

C:Accession: S69339; S72664

R:Khamlich, A.A.; Aucoctuer, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687; PMID:7744049

A:Accession: S69339

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

A:Cross-references: UNIPARC:UPI0000176F24; EMBL:X81695

R:Khamlich, A.A.

submitted to the EMBL Data Library, September 1994

A:Reference number: S72664

A:Accession: S72664

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-140,'C','142-374 <KH2>

A:Cross-references: UNIPARC:UPI0000176F25; EMBL:X81695

C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 99.1%; Score 1227; DB 2; Length 374;
Best Local Similarity 99.1%; Pred. No. 2, 7e-88;

Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 DKHTCPPCPAPELLGSPVFLFPPKXDTLMSRTPEVTCVVVDVSHEDPEVKFNYYVD 61
Db 148 DKHTCPPCPAPELLGSPVFLFPPKXDTLMSRTPEVTCVVVDVSHEDPEVKFNYYVD 207
Qy 62 GVEVHNAKTKRREQNSTRVSVLTFLVDWNGKEYCKVSNKALPAPIETISKAK 121
Db 208 GVEVHNAKTKRREQNSTRVSVLTFLVDWNGKEYCKVSNKALPAPIETISKAK 267

QY 122 GQREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 181
 |||
 DB 268 GQREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 327
 |||
 QY 182 DGSFPLYSKLTVDKSRWQGNVSCSVMEALHNHYTKSLSPGK 228
 |||
 DB 328 DGSFPLYSKLTVDKSRWQGNVSCSVMEALHNHYTKSLSPGK 374
 |||

RESULT 4

PT0207
 Ig gamma chain C region - chimpanzee
 C/Species: Pan troglodytes (chimpanzee)
 C/Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
 R/Accession: PT0207
 R/Enrich: P.H.; Moustafa, Z.A.; Oestberg, L.
 Mol. Immunol. 28, 319-322, 1991
 A/Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
 A/Reference number: PT0207; MUID:9128716; PMID:2062315
 A/Accession: PT0207
 A/Molecule type: mRNA
 A/Residues: 1-234 <EHR>
 A/Cross-references: UNIPARC:UPI0000176F05
 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: immunoglobulin
 P/48-117/Domain: immunoglobulin homology <IMM>

Query Match 95.3%; Score 1180; DB 2; Length 234;
 Best Local Similarity 98.6%; Pred. No. 7e-85;
 Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 DKHTPCPCAPRLGSPVFLFPPPKDITMTSRTPEVTCVVDVSHEDPEVKFNYYVD 61
 |||
 DB 15 DTHHTPCPCAPRLGSPVFLFPPPKDITMTSRTPEVTCVVDVSHEDPEVKFNYYVD 74
 |||
 QY 62 GVEVHNAKTPREBQYNSTRVSVLTVLHODWLNKGEYCKVSNKALPAPIETISKAK 121
 |||
 DB 75 GVEVHNAKTPREBQYNSTRVSVLTVLHODWLNKGEYCKVSNKALPAPIETISKAK 134
 |||
 QY 122 GQREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 181
 |||
 DB 135 GQREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 194
 |||
 QY 182 DGSFPLYSKLTVDKSRWQGNVSCSVMEALHNHYTKS 221
 |||
 DB 195 DGSFPLYSKLTVDKSRWQGNVSCSVMEALHNHYTKS 234
 |||

RESULT 5

A23511
 Ig gamma-3 chain C region (allotype G3m(b)) - human
 C/Species: Homo sapiens (man)
 C/Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999
 C/Accession: A23511
 R/Huck, S.; Port, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.
 Nucleic Acids Res. 14, 1779-1789, 1986
 A/Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: cc
 A/Reference number: A23511; MUID:86148507; PMID:3081877
 A/Accession: A23511
 A/Molecule type: DNA
 A/Residues: 1-377 <HUC>
 A/Cross-references: UNIPARC:UPI000004718F; GB:X03604; GB:M12358; NID:g33070; PIND:CAA272

C/Genetic:
 A/Gene: GDB:IGHG3
 A/Cross-references: GDB:119339; OMIM:147120
 A/Map position: 14q32.33-14q32.33
 A/Intons: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3
 C/Superfamily: immunoglobulin C region; immunoglobulin homology
 C/Keywords: immunoglobulin
 P/20-85/Domain: immunoglobulin homology <IMM>

Query Match 92.6%; Score 1146; DB 2; Length 377;
 Best Local Similarity 92.5%; Pred. No. 5.7e-82;

Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
 QY 2 DKHTPCPCAPRLGSPVFLFPPPKDITMTSRTPEVTCVVDVSHEDPEVKFNYYVD 61
 |||
 DB 151 DTHHTPCPCAPRLGSPVFLFPPPKDITMTSRTPEVTCVVDVSHEDPEVKFNYYVD 210
 |||
 QY 62 GVEVHNAKTPREBQYNSTRVSVLTVLHODWLNKGEYCKVSNKALPAPIETISKAK 121
 |||
 DB 211 GVEVHNAKTPREBQYNSTRVSVLTVLHODWLNKGEYCKVSNKALPAPIETISKAK 270
 |||
 QY 122 GQREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 181
 |||
 DB 271 GQREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 330
 |||
 QY 182 DGSFPLYSKLTVDKSRWQGNVSCSVMEALHNHYTKSLSPGK 228
 |||
 DB 331 DGSFPLYSKLTVDKSRWQGNVSCSVMEALHNHYTKSLSPGK 377
 |||

RESULT 6

A60764
 Ig gamma-3 chain C region, form IAT - human
 C/Species: Homo sapiens (man)
 C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 31-Dec-2004
 C/Accession: A60764
 R/Huck, S.; Lefranc, G.; Lefranc, M.P.
 Immunogenetics 30, 250-257, 1989
 A/Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 convert
 A/Reference number: A60764; MUID:90007613; PMID:2571587
 A/Accession: A60764
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-377 <HUC>
 A/Cross-references: UNIPROT:Q8N4Y9; UNIPARC:UPI0000176F08
 C/Superfamily: immunoglobulin homology
 C/Keywords: immunoglobulin
 P/20-85/Domain: immunoglobulin homology <IMM>

Query Match 92.4%; Score 1144; DB 2; Length 377;
 Best Local Similarity 92.5%; Pred. No. 8.2e-82;
 Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

QY 2 DKHTPCPCAPRLGSPVFLFPPPKDITMTSRTPEVTCVVDVSHEDPEVKFNYYVD 61
 |||
 DB 151 DTHHTPCPCAPRLGSPVFLFPPPKDITMTSRTPEVTCVVDVSHEDPEVKFNYYVD 210
 |||
 QY 62 GVEVHNAKTPREBQYNSTRVSVLTVLHODWLNKGEYCKVSNKALPAPIETISKAK 121
 |||
 DB 211 GVEVHNAKTPREBQYNSTRVSVLTVLHODWLNKGEYCKVSNKALPAPIETISKAK 270
 |||
 QY 122 GQREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 181
 |||
 DB 271 GQREPPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVLD 330
 |||
 QY 182 DGSFPLYSKLTVDKSRWQGNVSCSVMEALHNHYTKSLSPGK 228
 |||
 DB 331 DGSFPLYSKLTVDKSRWQGNVSCSVMEALHNHYTKSLSPGK 377
 |||

RESULT 7

G2HU
 Ig gamma-2 chain C region - human
 C/Species: Homo sapiens (man)
 C/Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 09-Jul-2004
 C/Accession: A93906; A92809; A90752; A93132; A02148
 R/Ellison, J.; Hood, L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
 A/Title: linkage and sequence homology of two human immunoglobulin gamma heavy chain com
 A/Reference number: A93906; MUID:82157621; PMID:6804948
 A/Accession: A93906
 A/Molecule type: DNA
 A/Residues: 1-326 <ELL>
 A/Cross-references: UNIPROT:P01859; UNIPARC:UPI000003BFFC; GB:V00554; GB:J00230; NID:g327

```

A:Note: Lys-32 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
U: Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and functional aspects
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein T11
A:Accession: A92809
A:Molecule type: protein
A:Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <MAN>
A:Cross-references: UNIPARC:UPI0000173791
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a human IgG2 heavy chain
A:Reference number: A90752; MUID:80001357; PMID:111060
A:Contents: myeloma protein Z1e
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-200, 'E', 202-203, 'E', 205-206, 'E', 208-209, 'E', 211-212, 'E', 214-215, 'E', 217-218, 'E', 220-221, 'E', 223-224, 'E', 226-227, 'E', 229-230, 'E', 232-233, 'E', 235-236, 'E', 238-239, 'E', 241-242, 'E', 244-245, 'E', 247-248, 'E', 250-251, 'E', 253-254, 'E', 256-257, 'E', 259-260, 'E', 262-263, 'E', 265-266, 'E', 268-269, 'E', 271-272, 'E', 274-275, 'E', 277-278, 'E', 280-281, 'E', 283-284, 'E', 286-287, 'E', 289-290, 'E', 292-293, 'E', 295-296, 'E', 298-299, 'E', 301-302, 'E', 304-305, 'E', 307-308, 'E', 310-311, 'E', 313-314, 'E', 316-317, 'E', 319-320, 'E', 322-323, 'E', 325-326, 'E', 328-329, 'E', 331-332, 'E', 334-335, 'E', 337-338, 'E', 340-341, 'E', 343-344, 'E', 346-347, 'E', 349-350, 'E', 352-353, 'E', 355-356, 'E', 358-359, 'E', 361-362, 'E', 364-365, 'E', 367-368, 'E', 370-371, 'E', 373-374, 'E', 376-377, 'E', 379-380, 'E', 382-383, 'E', 385-386, 'E', 388-389, 'E', 391-392, 'E', 394-395, 'E', 397-398, 'E', 400-401, 'E', 403-404, 'E', 406-407, 'E', 409-410, 'E', 412-413, 'E', 415-416, 'E', 418-419, 'E', 421-422, 'E', 424-425, 'E', 427-428, 'E', 430-431, 'E', 433-434, 'E', 436-437, 'E', 439-440, 'E', 442-443, 'E', 445-446, 'E', 448-449, 'E', 451-452, 'E', 454-455, 'E', 457-458, 'E', 460-461, 'E', 463-464, 'E', 466-467, 'E', 469-470, 'E', 472-473, 'E', 475-476, 'E', 478-479, 'E', 481-482, 'E', 484-485, 'E', 487-488, 'E', 490-491, 'E', 493-494, 'E', 496-497, 'E', 499-500, 'E', 502-503, 'E', 505-506, 'E', 508-509, 'E', 511-512, 'E', 514-515, 'E', 517-518, 'E', 520-521, 'E', 523-524, 'E', 526-527, 'E', 529-530, 'E', 532-533, 'E', 535-536, 'E', 538-539, 'E', 541-542, 'E', 544-545, 'E', 547-548, 'E', 550-551, 'E', 553-554, 'E', 556-557, 'E', 559-560, 'E', 562-563, 'E', 565-566, 'E', 568-569, 'E', 571-572, 'E', 574-575, 'E', 577-578, 'E', 580-581, 'E', 583-584, 'E', 586-587, 'E', 589-590, 'E', 592-593, 'E', 595-596, 'E', 598-599, 'E', 601-602, 'E', 604-605, 'E', 607-608, 'E', 610-611, 'E', 613-614, 'E', 616-617, 'E', 619-620, 'E', 622-623, 'E', 625-626, 'E', 628-629, 'E', 631-632, 'E', 634-635, 'E', 637-638, 'E', 640-641, 'E', 643-644, 'E', 646-647, 'E', 649-650, 'E', 652-653, 'E', 655-656, 'E', 658-659, 'E', 661-662, 'E', 664-665, 'E', 667-668, 'E', 670-671, 'E', 673-674, 'E', 676-677, 'E', 679-680, 'E', 682-683, 'E', 685-686, 'E', 688-689, 'E', 691-692, 'E', 694-695, 'E', 697-698, 'E', 700-701, 'E', 703-704, 'E', 706-707, 'E', 709-710, 'E', 712-713, 'E', 715-716, 'E', 718-719, 'E', 721-722, 'E', 724-725, 'E', 727-728, 'E', 730-731, 'E', 733-734, 'E', 736-737, 'E', 739-740, 'E', 742-743, 'E', 745-746, 'E', 748-749, 'E', 751-752, 'E', 754-755, 'E', 757-758, 'E', 760-761, 'E', 763-764, 'E', 766-767, 'E', 769-770, 'E', 772-773, 'E', 775-776, 'E', 778-779, 'E', 781-782, 'E', 784-785, 'E', 787-788, 'E', 790-791, 'E', 793-794, 'E', 796-797, 'E', 799-800, 'E', 802-803, 'E', 805-806, 'E', 808-809, 'E', 811-812, 'E', 814-815, 'E', 817-818, 'E', 820-821, 'E', 823-824, 'E', 826-827, 'E', 829-830, 'E', 832-833, 'E', 835-836, 'E', 838-839, 'E', 841-842, 'E', 844-845, 'E', 847-848, 'E', 850-851, 'E', 853-854, 'E', 856-857, 'E', 859-860, 'E', 862-863, 'E', 865-866, 'E', 868-869, 'E', 871-872, 'E', 874-875, 'E', 877-878, 'E', 880-881, 'E', 883-884, 'E', 886-887, 'E', 889-890, 'E', 892-893, 'E', 895-896, 'E', 898-899, 'E', 901-902, 'E', 904-905, 'E', 907-908, 'E', 910-911, 'E', 913-914, 'E', 916-917, 'E', 919-920, 'E', 922-923, 'E', 925-926, 'E', 928-929, 'E', 931-932, 'E', 934-935, 'E', 937-938, 'E', 940-941, 'E', 943-944, 'E', 946-947, 'E', 949-950, 'E', 952-953, 'E', 955-956, 'E', 958-959, 'E', 961-962, 'E', 964-965, 'E', 967-968, 'E', 970-971, 'E', 973-974, 'E', 976-977, 'E', 979-980, 'E', 982-983, 'E', 985-986, 'E', 988-989, 'E', 991-992, 'E', 994-995, 'E', 997-998, 'E', 1000-1001, 'E', 1003-1004, 'E', 1006-1007, 'E', 1009-1010, 'E', 1012-1013, 'E', 1015-1016, 'E', 1018-1019, 'E', 1021-1022, 'E', 1023-1024, 'E', 1026-1027, 'E', 1029-1030, 'E', 1032-1033, 'E', 1035-1036, 'E', 1038-1039, 'E', 1041-1042, 'E', 1044-1045, 'E', 1047-1048, 'E', 1050-1051, 'E', 1053-1054, 'E', 1056-1057, 'E', 1059-1060, 'E', 1062-1063, 'E', 1065-1066, 'E', 1068-1069, 'E', 1071-1072, 'E', 1074-1075, 'E', 1077-1078, 'E', 1080-1081, 'E', 1083-1084, 'E', 1086-1087, 'E', 1089-10
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```

Oy      127  PoyVTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEKESNGQPENNYKTTPPVLDSDGSFF  186
          |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      225  PoyVTLPPSRRESMTKNQVSLTCLVKGFYPSDIAVEKESNGQPENNYKTTPPMLDSGDSFF  284

Oy      187  LYSKLTVDKSRWQGQNVFSCSVMEHALHNHYTKSLSLSPGK  228
Db      285  LYSKLTVDKSRWQGQNVFSCSVMEHALHNHYTKSLSLSPGK  326

RESULT 8
G4HU
Ig gamma-4 chain C region - human
CISpecies: Homo sapiens (man)
CIDate: 02-Apr-1982 #sequence revision 02-Apr-1982 #ext_change 09-Jul-2004
CIAccession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A>Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
AReference number: A90933; MUID:83157104; PMID:6299662
AAccession: A90933
A:Molecule type: DNA
A:Residues: 1-327 <ELI>
A:Cross-references: UNIPROT:P01861; UNIPARC:UPI0000047190
A>Note: The sequence was determined from the germline gene
B:Pink, J.R.L., Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A>Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant re
AAccession: A90249; MUID:70207560; PMID:4192699
A:Molecule type: protein
A:Residues: 1-30;81-326 <PIN>
A:Cross-references: UNIPARC:DPI0000173795; UNIPARC:UPI0000173796
C:Genetics:
A:Gene: GDB:IGHG4
A:Cross-references: GDB:119340; OMIM:147130
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1, 111/1, 221/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into lar
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IMI>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83,141-201,247-305/Disulfide bonds: #status predicted
F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match          91.7%; Score 1135; DB 1; Length 327;
Best Local Similarity 93.7%; Pred. No. 3,4e-81;
Matches 208; Conservative 8; Mismatches 6; Indels 0; Gaps. 0;

Oy      7  CPPCPAPELLGGBSVFLLFPPEKDTLMISRTPEVTCVVVDVSHPEDPKENVYDGVEH  66
          |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     106  CPSCPAPBELGGBSVFLLFPPEKDTLMISRTPEVTCVVVDVSODPEQFNMYVDGEVH  165

Oy     67  NAKTPREQGVNSTRVAVSLVTLLHODMLNKGKKCVSKALPAPEKTIISKAGQPRE  126
          |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db     166  NAKTPREQGFNSTRVAVSLVTLLHODMLNKGKKCVSKGLPSSLEKTIISKAGQPRE  225

Oy    127  PoyVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEKESNGQPENNYKTTPPVLDSDGSFF  186
          |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    226  PoyVTLPPSQEREMTKNQVSLTCLVKGFYPSDIAVEKESNGQPENNYKTTPPVLDSDGSFF  285

Oy    187  LYSKLTVDKSRWQGQNVFSCSVMEHALHNHYTKSLSLSPGK  228
          |||||:::||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    286  LYSRLTVDKSRWQGNVFCFSVMHEALHNHYTKSLSLSPGK  327

RESULT 9
```


A:Accession: A94553
 A:Molecule type: protein
 A:Residues: 1-3 <TR1>
 A:Cross-reference: UNIPROT:P01862; UNIPARC:UPI000017379E
 R:Birnstein, B.K.; Hussain, Q.Z.; Cebra, J.J.
 Biochemistry 10, 18-25, 1971
 A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Am
 A:Reference number: A90352; MUID:71058471; PMID:5538606
 A:Accession: A90352
 A:Molecule type: protein
 A:Residues: 4-68 <BIR>
 A:Cross-reference: UNIPARC:UPI000017379F
 R:Turner, K.J.; Cebra, J.J.
 Biochemistry 10, 9-17, 1971
 A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am
 A:Reference number: A90359; MUID:71058486; PMID:5538616
 A:Accession: A90359
 A:Molecule type: protein
 A:Residues: 69-133/312-329 <TUR>
 A:Cross-reference: UNIPARC:UPI00001737A0; UNIPARC:UPI00001737A1
 R:Tracey, D.E.; Cebra, J.J.
 Biochemistry 13, 4796-4803, 1974
 A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.
 A:Reference number: A90384; MUID:75036072; PMID:4429665
 A:Accession: A90384
 A:Molecule type: protein
 A:Residues: 134-226 <TRA>
 A:Cross-reference: UNIPARC:UPI00001737A2
 R:Trischmann, T.M.; Cebra, J.J.
 Biochemistry 13, 4804-4811, 1974
 A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.
 A:Reference number: A90385; MUID:75036073; PMID:4609467
 A:Accession: A90385
 A:Molecule type: protein
 A:Residues: 227-311 <TR2>
 A:Cross-reference: UNIPARC:UPI00001737A3
 R:Oliveira, B.; Lamm, M.E.
 Biochemistry 10, 26-31, 1971
 A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.
 A:Reference number: A90354; MUID:71058474; PMID:4925544
 A:Contents: annotation; disulfide bonds
 A:Note: Cys-16 is involved in a heavy-light chain bond
 A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
 C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:21-81/Domain: immunoglobulin homology <IM1>
 F:135-204/Domain: immunoglobulin homology <IM2>
 F:241-310/Domain: immunoglobulin homology <IM3>
 F:28-79/Disulfide bonds: #status experimental
 F:142-202/Disulfide bonds: #status experimental
 F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
 F:248-308/Disulfide bonds: #status experimental

Query Match 71.8%; Score 889; DB 1; Length 329;
 Best Local Similarity 72.3%; Pred. No. 5.3e-62;
 Matches 162; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

6 TCPCPAPBELLGGPSVFLPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDQVEV 65
 106 TCPCPAPBELLGGPSVFLPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDQVEV 165
 66 HNAKTRERQVNSTYRVSVLTGLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPR 125
 166 GNAETKPRVQVNTTFVRSVLTGLHODWLNKGYKCKVSNKALPAPIEKTISKAKGAPR 225
 126 EPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVENSNGQ--ENNYYKTPPVLDSDG 183
 226 MPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVENSNGQ--ENNYYKTPPVLDSDG 285
 184 SFPLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPG 227

Db 286 SYPLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPG 329
 RESULT 15
 147158
 Ig gamma 1 chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: I47158
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
 A:Reference number: I47158; MUID:95015845; PMID:7930579
 A:Accession: I47158
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-reference: UNIPARC:UPI0000115523; EMBL:U03378; NID:9433121; PIDN:AAA52216.1; PII
 C:GeneticB:
 A:Gene: IgG1
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IM>

Query Match 71.5%; Score 885.5; DB 2; Length 328;
 Best Local Similarity 72.4%; Pred. No. 1e-61;
 Matches 163; Conservative 27; Mismatches 32; Indels 3; Gaps 2;

6 TCPCPAPBELLGGPSVFLPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDQVEV 65
 105 TCPCPAPBELLGGPSVFLPPKPKDITLMSRTPEVTCVVVDVSHEDPEVKFNMYVDQVEV 163
 66 HNAKTRERQVNSTYRVSVLTGLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPR 125
 164 HTAETKPRVQVNTTFVRSVLTGLHODWLNKGYKCKVSNKALPAPIEKTISKAKGQPR 223
 126 EPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVENSNGQ--ENNYYKTPPVLDSDG 183
 224 EPQVYTLPPSRDELTKQVSLTCLVKGFPSPDIAVENSNGQ--ENNYYKTPPVLDSDG 283
 184 SFPLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPG 228
 284 TFFLYSKLTVDKSRWQGNVFSVSMHEALHNHYTQKSLSLSPG 328

Search completed: March 16, 2006, 20:05:20
 Job time: 41 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 16, 2006, 19:57:23 ; Search time 228 Seconds
(without alignments)
705.528 Million cell updates/sec

Title: US-10-609-217-2
Perfect score: 1238
Sequence: 1 MDKTHCPPCPAPRLGSPS.....MHEALHNHYTKSLSLSPGR 228

Scoring table: BIOSUM62
Gap 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Datebase : Uniprot 05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	99.6	330	1	IGHG1_HUMAN
2	1233	99.6	465	2	OGGMX6_HUMAN
3	1233	99.6	466	2	OGIN78_HUMAN
4	1233	99.6	469	2	OG59F4_HUMAN
5	1233	99.6	469	2	Q7Z7P5_HUMAN
6	1233	99.6	470	2	Q7Z5W1_HUMAN
7	1233	99.6	470	2	OGPJ44_HUMAN
8	1233	99.6	472	2	OGN089_HUMAN
9	1233	99.6	475	2	OGEPF5_HUMAN
10	1233	99.6	475	2	OGGMW7_HUMAN
11	1233	99.6	476	2	OGGMX1_HUMAN
12	1233	99.6	479	2	OG6P08_HUMAN
13	1229	99.3	473	2	OGP055_HUMAN
14	1229	99.3	475	2	OGMZ06_HUMAN
15	1229	99.3	480	2	OGN094_HUMAN
16	1229	99.3	481	2	OGN097_HUMAN
17	1229	99.3	482	2	Q7Z351_HUMAN
18	1227	99.1	473	2	OGPYX1_HUMAN
19	1227	99.1	473	2	OGMZV7_HUMAN
20	1227	99.1	478	2	OGPI81_HUMAN
21	1227	99.1	480	2	OGPJF1_HUMAN
22	1226	99.0	466	2	OGN096_HUMAN
23	1222	98.7	475	2	OGN095_HUMAN
24	1222	98.7	544	2	OGPJ95_HUMAN
25	1216	98.2	487	2	OGSZL2_HUMAN
26	1172	94.7	475	2	OGSR17_HUMAN
27	1146	92.6	354	2	OG6TT2_HUMAN
28	1146	92.6	518	2	OGN030_HUMAN
29	1146	92.6	519	2	OGEBM2_HUMAN
30	1142.5	92.3	326	1	IGHG2_HUMAN
31	1142.5	92.3	417	2	OGN093_HUMAN

32	1142	92.2	521	2	OGN4Y9_HUMAN	OGN4Y9 homo sapien
33	1139.5	92.0	464	2	OGMZU6_HUMAN	OGMZU6 homo sapien
34	1137.5	91.9	465	2	OGP6C4_HUMAN	OGP6C4 homo sapien
35	1135	91.7	327	1	IGHG4_HUMAN	IGHG4 homo sapien
36	1135	91.7	473	2	OGTC63_HUMAN	OGTC63 homo sapien
37	1131	91.4	509	2	OGNFI7_HUMAN	OGNFI7 homo sapien
38	1128.5	91.2	470	2	OG6CN4_HUMAN	OG6CN4 homo sapien
39	1126	91.0	290	1	IGHG3_HUMAN	IGHG3 homo sapien
40	1126	91.0	476	2	OGMZX7_HUMAN	OGMZX7 homo sapien
41	918.5	74.2	323	1	GC_RABIT	P01870 oryctolagus
42	909	73.4	337	2	Q95M34_HORSE	Q95M34 equus caball
43	889	71.8	329	1	IGHG2_CAVPO	P01862 cavia porcea
44	845.5	68.3	329	1	GC3_MOUSE	P22436 mus musculus
45	845.5	68.3	470	2	Q7TMK1_MOUSE	Q7TMK1 mus musculus

ALIGNMENTS

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RESULT 1
IGHG1_HUMAN
ID IGHG1_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE I9 gamma-1 chain C region.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
CX NCBI_TaxID=9606;
[1]
NUCLEOTIDE SEQUENCE.
RP MEDLINE=82274238; PubMed=6287432;
RA Ellison J.W., Berson B.J., Hood L.B.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
[2]
PROTEIN SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RP MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Wardal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RL acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RN Biochemistry 9:3161-3170(1970).
[3]
PROTEIN SEQUENCE OF 136-329 (EU).
RP MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RL acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RN Biochemistry 9:3171-3181(1970).
[4]
PROTEIN SEQUENCE (MYELOMA PROTEIN NIE).
RP MEDLINE=77070269; PubMed=826475;
RA Ponsztynski H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a monoclonal
RL IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic
RT peptides of the H-chain, alignment of the tryptic peptides and
RL discussion of the complete structure.";
RN Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
[5]
PROTEIN SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RP MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.B., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RL structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RN Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
[6]
DISULFIDE BONDS.

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RX MEDLINE=71064027; PubMed=4923144;
 RA Gall W.E., Edelman G.M.;
 RT "the covalent structure of a human gamma G-immunoglobulin. X.
 RT Intrachain disulfide bonds.";
 RL Biochemistry 9:3188-3196 (1970).
 RN [7]
 RP DISULFIDE BONDS.
 RX MEDLINE=77070267; PubMed=1002129;
 RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT IgG1 immunoglobulin (myeloma protein N1e), I: purification and
 RT characterization of the protein, the L- and H-chains, the cyanogen
 RT bromide cleavage products, and the disulfide bridges.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540 (1976).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
 RX MEDLINE=81208100; PubMed=7236608;
 RA Dessenhofer J.;
 RT "Crystallographic refinement and atomic models of a human Fc fragment
 RT and its complex with fragment B of protein A from *Staphylococcus*
 RT aureus at 2.9- and 2.8-A resolution.";
 RL Biochemistry 20:2361-2370 (1981)
 CC -1- MISCELLANEOUS: N1e has the G1M(17) allotypic marker, 97-K, and the
 CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
 CC G1M(3) marker and the G1M (non-1) markers.
 CC -1- MISCELLANEOUS: N1e also differs in the amidation states of 35,
 CC 116, 198, 269 and 272.
 CC -1- MISCELLANEOUS: EU also differs in the amidation states of residues
 CC 155, 166, 177, 195, 196, 269, and 272 and in the order of residues
 CC 268-272.
 CC -1- MISCELLANEOUS: KOL also differs in the amidation states of
 CC residues 198, 267 and 272.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL: J00928; AAC82527.1; ALT_INIT; Genomic_DNA.
 DR PIR: A93433; GHHD.
 DR PDB: 1AJ7; X-ray; H=1-103.
 DR PDB: 1AOK; X-ray; H=1-103.
 DR PDB: 1DSB; X-ray; B/H=1-101.
 DR PDB: 1DS1; X-ray; H=1-101.
 DR PDB: 1D6V; X-ray; H=1-101.
 DR PDB: 1DN2; X-ray; A/B=120-326.
 DR PDB: 1E4K; X-ray; A/B=106-330.
 DR PDB: 1FC1; X-ray; A/B=106-329.
 DR PDB: 1FC2; X-ray; D=106-329.
 DR PDB: 1FCC; X-ray; A=121-326.
 DR PDB: 1H2H; X-ray; H/K=1-330.
 DR PDB: 1I7Z; X-ray; B/D=1-103.
 DR PDB: 1IIS; X-ray; A/B=107-330.
 DR PDB: 1IIX; X-ray; A/B=107-330.
 DR PDB: 1L6X; X-ray; A=120-326.
 DR PDB: 1QOX; X-ray; A/B=119-330.
 DR PDB: 1T83; X-ray; A/B=107-330.
 DR PDB: 2RCS; X-ray; H=1-103.
 DR HGNC: HGNC:5525; IGHG1.
 DR MIM: 147100; -.
 DR GO: GO:0005624; C:membrane fraction; NAS.
 DR GO: GO:0003823; F:antigen binding; TAS.
 DR GO: GO:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003597; Ig_c1.
 DR InterPro: IPR003006; IG_MHC.
 DR Pfam: PF07654; C1-set; 3.
 DR PROSITE: PS50835; IG_LIKE; 3.
 DR PROSITE: PS00290; IG_MHC; 2.
 DR 3D-structure; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin C region; Immunoglobulin domain.
 FT REGION 1 98 CH1.

FT REGION 99 110 Hinge.
 FT REGION 111 223 CH2.
 FT REGION 224 330 CH3.
 FT CARBOHYD 180 180 N-linked (GlcNAc...).
 FT DISULFID 27 83 Interchain (with light chain).
 FT DISULFID 103 103 Interchain (with heavy chain).
 FT DISULFID 109 109 Interchain (with heavy chain).
 FT DISULFID 112 112 Interchain (with heavy chain).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT NON_TER 1 1
 FT STRAND 23 24
 FT STRAND 26 33
 FT STRAND 38 38
 FT STRAND 41 41
 FT STRAND 42 45
 FT TURN 48 49
 FT STRAND 50 52
 FT STRAND 57 58
 FT TURN 59 61
 FT STRAND 62 71
 FT STRAND 73 75
 FT HELIX 76 78
 FT TURN 82 87
 FT STRAND 88 91
 FT TURN 92 97
 FT TURN 102 103
 FT STRAND 122 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 149
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 167
 FT STRAND 171 172
 FT STRAND 176 177
 FT TURN 179 180
 FT STRAND 183 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 207
 FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 242
 FT STRAND 245 256
 FT STRAND 261 266
 FT TURN 267 268
 FT STRAND 269 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 306 311
 FT TURN 313 314
 FT HELIX 316 318
 FT STRAND 319 324
 SQ SEQUENCE 330 AA; 36106 MW; 3770EB106C2PA33D CRC64;
 Query Match 99.6%; Score 1233; DB 1; Length 330;
 Best Local Similarity 100.0%; Pred. No. 5,8e-92;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 DKHTCPCCPAPBLIGBSVFLFPPKPKDTIMISRTBEVTCVVVDVSHEDPEVKFNMYVD 61

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Db      104 DKHTCPCPAPBELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVFENYVD 163
Qy      62 GVEVHNAKTKPRREQNSTRVYVSFLVTLVHODMNLNGEKYCKVKSNKALPAIETKISKAK 121
Db      164 GVEVHNAKTKPRREQNSTRVYVSFLVTLVHODMNLNGEKYCKVKSNKALPAIETKISKAK 223
Qy      122 GQRPBPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLD 181
Db      224 GQRPBPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLD 283
Qy      182 DGSFFLYSKLTVDSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 228
Db      284 DGSFFLYSKLTVDSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 330

RESULT 2
OG6MX6 HUMAN PRELIMINARY; PRT; 465 AA.
ID OG6MX6
AC OG6MX6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR GO; GO:0016021; C:Integral to membrane; IEA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR Hydrophobic protein.
KW SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDBJ386E CRC64;
SQ

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Query Match      99.6%; Score 1233; DB 2; Length 465;
Best Local Similarity 100.0%; Pred. No. 9e-92;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 DKHTCPCPAPBELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVFENYVD 61.
Db      239 DKHTCPCPAPBELLGGPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVFENYVD 298
Qy      62 GVEVHNAKTKPRREQNSTRVYVSFLVTLVHODMNLNGEKYCKVKSNKALPAIETKISKAK 121
Db      299 GVEVHNAKTKPRREQNSTRVYVSFLVTLVHODMNLNGEKYCKVKSNKALPAIETKISKAK 358
Qy      122 GQRPBPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLD 181
Db      359 GQRPBPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTTPVLD 418

Qy      182 DGSFFLYSKLTVDSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 228
Db      419 DGSFFLYSKLTVDSRWQGNVFCSCVMEALHNHYTQKSLSLSPGK 465

RESULT 3
OG1N78 HUMAN PRELIMINARY; PRT; 466 AA.
ID OG1N78
AC OG1N78
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshitoki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RG NIH MGC Project;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; mRNA.
DR HSSP; P01861; IAD0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.

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DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGCL; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 DR SEQUENCE 466 AA; 50854 MW; 53EB0BCDEB810765 CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 466;
 Best Local Similarity 100.0%; Pred. No. 9e-92;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61
 DB 240 DKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 299
 QY 62 GVEVHNAKTRERQYNSTRVSVLTVLHODWLNKGKCKVSNKALPAPIETKISKAK 121
 DB 300 GVEVHNAKTRERQYNSTRVSVLTVLHODWLNKGKCKVSNKALPAPIETKISKAK 359
 QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
 DB 360 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 419
 QY 182 DGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
 DB 420 DGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 466

RESULT 4

OS 0569F4 HUMAN PRELIMINARY; PRT; 469 AA.

AC Q569F4;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
 DE IGHG1 protein.

GN Name=IGHG1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

NCBI_TaxID=9606;

NP NUCLEOTIDE SEQUENCE.

RC TISSUE=lymph;

RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshlyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=lymph;
 RG NIH MGC Project;

RL Submitted (Apr-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC092518; AAH92518.1; -; mRNA.

DR SEQUENCE 469 AA; 51254 MW; AC13448B3047784F CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 469;
 Best Local Similarity 100.0%; Pred. No. 9.1e-92;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61
 DB 243 DKHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 302
 QY 62 GVEVHNAKTRERQYNSTRVSVLTVLHODWLNKGKCKVSNKALPAPIETKISKAK 121
 DB 303 GVEVHNAKTRERQYNSTRVSVLTVLHODWLNKGKCKVSNKALPAPIETKISKAK 362
 QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 181
 DB 363 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLD 422
 QY 182 DGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
 DB 423 DGSFPLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK 469

RESULT 5

OS 0727P5 HUMAN PRELIMINARY; PRT; 469 AA.

AC Q727P5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHG1 protein.

GN Name=IGHG1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

NCBI_TaxID=9606;

NP NUCLEOTIDE SEQUENCE.

RC TISSUE=Spleen;

RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshlyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;

RG NIH MGC Project;

RL Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC051328; AAH51328.1; -; mRNA.

DR HSSP; P01857; IGH.

DR SMR; Q727P5; 20-469.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG-cl.

DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF07654; Cl-sec; 3.

DR EMBL; BC018747; AAH18747.1; -; mRNA.
 DR HSP; P01861; IADQ.
 DR SMR; O6RJA4; 20-470.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 DR SEQUENCE 470 AA; 51716 MW; 7B49556A11FD7D99 CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 470;
 Best Local Similarity 100.0%; Pred. No. 9.1e-92;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61
 DB 244 DKHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 303
 QY 62 GVEVHNAKTKRREQDYNSTRVSVLTLYHODMNLGKEYCKCKVSNKALPAPIEKTISKAK 121
 DB 304 GVEVHNAKTKRREQDYNSTRVSVLTLYHODMNLGKEYCKCKVSNKALPAPIEKTISKAK 363
 QY 122 GQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPVLD 181
 DB 364 GQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPVLD 423
 QY 182 DGSFFLYSKLTVDKSRMGOQGVNFSCVMHEALHNHYTOKSLSLSPGK 228
 DB 424 DGSFFLYSKLTVDKSRMGOQGVNFSCVMHEALHNHYTOKSLSLSPGK 470

RESULT 8

Q6N089 HUMAN PRELIMINARY; PRT; 472 AA.

AC Q6N089; 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686P15220.
 GN Name=DKFZp686P15220;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Rectum tumor;
 RG The German cDNA Consortium;
 RA Wambut R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wilmann S.;
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640627; CAB45781.1; -; mRNA.
 DR HSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 KW Hypothetical protein.
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 472;
 Best Local Similarity 100.0%; Pred. No. 9.2e-92;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61
 DB 246 DKHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 305
 QY 62 GVEVHNAKTKRREQDYNSTRVSVLTLYHODMNLGKEYCKCKVSNKALPAPIEKTISKAK 121
 DB 306 GVEVHNAKTKRREQDYNSTRVSVLTLYHODMNLGKEYCKCKVSNKALPAPIEKTISKAK 365
 QY 122 GQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPVLD 181
 DB 366 GQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPVLD 425
 QY 182 DGSFFLYSKLTVDKSRMGOQGVNFSCVMHEALHNHYTOKSLSLSPGK 228
 DB 426 DGSFFLYSKLTVDKSRMGOQGVNFSCVMHEALHNHYTOKSLSLSPGK 472

RESULT 9

Q5EFES HUMAN PRELIMINARY; PRT; 475 AA.

AC Q5EFES; 10-MAY-2005 (Tremblrel. 30, Created)
 DT 10-MAY-2005 (Tremblrel. 30, Last sequence update)
 DT 10-MAY-2005 (Tremblrel. 30, Last annotation update)
 DE Anti-Rhd monoclonal T125 gamma1 heavy chain precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gaucher C., Klein P., Bellard R.;
 RT "Sequence determination of the recombinant human anti-Rhd monoclonal
 RT antibody T125."
 RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY894992; AAW62028.1; -; mRNA.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR Pfam; PF07686; V-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGcl; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 KW Signal.
 FT SIGNAL 1 19 Potential.
 FT CHAIN 20 475 anti-Rhd monoclonal T125 gamma1 heavy
 FT CHAIN chain.
 SQ SEQUENCE 475 AA; 52362 MW; 1367D400DC7D2859 CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 475;
 Best Local Similarity 100.0%; Pred. No. 9.3e-92;
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61
 DB 249 DKHTCPCPAPPELLGSPVFLPPPKKDTLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 308
 QY 62 GVEVHNAKTKRREQDYNSTRVSVLTLYHODMNLGKEYCKCKVSNKALPAPIEKTISKAK 121
 DB 309 GVEVHNAKTKRREQDYNSTRVSVLTLYHODMNLGKEYCKCKVSNKALPAPIEKTISKAK 368
 QY 122 GQPREPQVYTLPPSRDELITKNQVSLTCLVKGFPYSDIAVEMESNGQPENNYKTTTPVLD 181

Db 369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGNGPENNYKTTIPVLDS 428
Qy 182 DGSFPLYSKLTVDKSRNQQGVNFSQSYWMEALHNHYTKSLISLSPGK 228
Db 429 DGSFPLYSKLTVDKSRNQQGVNFSQSYWMEALHNHYTKSLISLSPGK 475

RESULT 10
ID 06GMW7_HUMAN PRELIMINARY; PRT; 475 AA.
AC 06GMW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=SpLeen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Valladao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=SpLeen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC073782; AAH73782.1; -, mRNA.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG-v.
DR Pfam: Pf07654; Cl-sec; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGC1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG LIKE; 4.
DR PROSITE: PSS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SSQUENCE 475 AA; 51987 MW; 2A1F55D73660F8 CRC64;

Qy 2 DKHTCPCPAPPELLGSPVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVKFNYYVD 61
Db 249 DKHTCPCPAPPELLGSPVFLFPKPKDITMISRTPEVTCVVVDVSHEDPEVKFNYYVD 308

Query Match 99.6%; Score 1233; DB 2; Length 475;
Best Local Similarity 100.0%; Pred. No. 9,3e-92;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 GVEYHNAKTPREROVNSTRYVSVLTLYLHODWLNGEKYCKKYSNKAIPAPIETKISKAK 121
Db 309 GVEYHNAKTPREROVNSTRYVSVLTLYLHODWLNGEKYCKKYSNKAIPAPIETKISKAK 366
Qy 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGNGPENNYKTTIPVLDS 181
Db 369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGNGPENNYKTTIPVLDS 428
Qy 182 DGSFPLYSKLTVDKSRNQQGVNFSQSYWMEALHNHYTKSLISLSPGK 228
Db 429 DGSFPLYSKLTVDKSRNQQGVNFSQSYWMEALHNHYTKSLISLSPGK 475

RESULT 11
ID 06GMX1_HUMAN PRELIMINARY; PRT; 476 AA.
AC 06GMX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=SpLeen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshyuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Valladao D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Paley J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Buttefield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=SpLeen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC073773; AAH73773.1; -, mRNA.
DR GO: GO:0016021; C:Integral to membrane; IEA.
DR InterPro: IPR003599; IG.
DR InterPro: IPR007110; IG-like.
DR InterPro: IPR003597; IG-cl.
DR InterPro: IPR003006; IG_MHC.
DR InterPro: IPR003596; IG-v.
DR Pfam: Pf07654; Cl-sec; 3.
DR SMART: SM00409; IG; 2.
DR SMART: SM00407; IGC1; 3.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PSS0835; IG LIKE; 4.
DR PROSITE: PSS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C63DDB9D CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 476;

Best Local Similarity 100.0%; Pred. No. 9.3e-92;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCPCPAPPELLGGPSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKFNNYVD 61
DB 250 DKHTCPCPAPPELLGGPSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKFNNYVD 309
QY 62 GVEVHNAKTRPREQYNSTRYVSVLTFLHQMVLNGEKYCKVSNKALPAPIEKTISKAK 121
DB 310 GVEVHNAKTRPREQYNSTRYVSVLTFLHQMVLNGEKYCKVSNKALPAPIEKTISKAK 369
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOEPENNYKTTIPVLD 181
DB 370 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOEPENNYKTTIPVLD 429
QY 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
DB 430 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 476

RESULT 12

Q96P08_HUMAN PRELIMINARY; PRT; 679 AA.

AC Q96P08; 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Factor VII active site mutant immunoconjugate.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21477446; PubMed=11593034; DOI=10.1073/pnas.201420298;
RA Hu Z., Garen A.;
RT "Targeting tissue factor on tumor vascular endothelial cells and tumor
RT cells for immunotherapy in mouse models of prostatic cancer.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE.

RA Hu Z., Garen A.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF272774; AAK5686.2; -; mRNA.
DR HSSP; P08709; IKLI.
DR SMK; Q96P08; 39-180, 191-444, 447-679.
DR Ensembl; ENSG00000057593; Homo sapiens.
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004263; F:chymotrypsin activity; IEA.
DR GO; GO:0004295; F:trypsin activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000152; Asx_hydroxyl_S.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001438; EGF_II.
DR InterPro; IPR006209; EGF_Like.
DR InterPro; IPR002383; GLA_blood.
DR InterPro; IPR007110; IG_Like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR001314; Peptidase_S1A.
DR InterPro; IPR001254; Peptidase_S1_S6.
DR InterPro; IPR000294; Vitk_dep_GLA.
DR Pfam; PF07654; Cl-sec; 2.
DR Pfam; PF00008; EGF; 1.
DR Pfam; PF00594; Gla; 1.
DR Pfam; PF00089; Trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PRINTS; PR00010; EGRBLOOD.
DR PRINTS; PR00001; GLABLOOD.
DR SMART; SM00179; EGF_CA; 1.

DR SMART; SM00069; GLA; 1.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00020; TRYP_SPC; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS50026; EGF_3; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00011; GLA_1; UNKNOWN_1.
DR PROSITE; PS50998; GLA_2; 1.
DR PROSITE; PS50835; IG_Like; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS50240; TRYPSIN_DOM; 1.
DR PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
SQ SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;

Query Match 99.6%; Score 1233; DB 2; Length 679;
Best Local Similarity 100.0%; Pred. No. 1.5e-91;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCPCPAPPELLGGPSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKFNNYVD 61
DB 453 DKHTCPCPAPPELLGGPSVFLPPPKKDTLMTSRTEPVTCVVVDVSHEDPEVKFNNYVD 512
QY 62 GVEVHNAKTRPREQYNSTRYVSVLTFLHQMVLNGEKYCKVSNKALPAPIEKTISKAK 121
DB 513 GVEVHNAKTRPREQYNSTRYVSVLTFLHQMVLNGEKYCKVSNKALPAPIEKTISKAK 572
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOEPENNYKTTIPVLD 181
DB 573 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOEPENNYKTTIPVLD 632
QY 182 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 228
DB 633 DGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 679

RESULT 13

O6P055_HUMAN PRELIMINARY; PRT; 473 AA.

AC Q6P055; 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derye J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhaly S.J.,
RA Bosak S.A., McGwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman W., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smalhus D.B.,
RA Scherch A., Schein J.E., Jones S.J.M., Merris M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Peripheral Nervous System;
RA Strauberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 99.3%; Score 1229; DB 2; Length 473;
Best Local Similarity 99.6%; Pred. No. 1.9e-91;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKHTCPCPAPBELLGGPSVFLPPPKKDTLMTSRTEVTCVVVDVSHEDPEVKFNMYVD 61
DB 247 DKHTCPCPAPBELLGGPSVFLPPPKKDTLMTSRTEVTCVVVDVSHEDPEVKFNMYVD 306

QY 62 GVEVHNAKTKRREQVSTYRVSVLTVLHODMNGEKYCKVNKAAPAEIKTISKAK 121
DB 307 GVEVHNAKTKRREQVSTYRVSVLTVLHODMNGEKYCKVNKAAPAEIKTISKAK 366

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTIPVLD 181
DB 367 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTIPVLD 426

QY 182 DGSFFLYSKLTVDKSRWQQGNVFCSVMEHGLNHYTQKSLISPGK 228
DB 427 DGSFFLYSKLTVDKSRWQQGNVFCSVMEHGLNHYTQKSLISPGK 473

RESULT 14
Q6MZ06_HUMAN PRELIMINARY; PRT; 475 AA.
AC Q6MZ06;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686g1190.
GN Name=DKFZp686g1190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Bahr A., Lauber J., Mewes H.W., Well B., Amid C., Osanger A., Fobo G.,
Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAE45972.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR SMR; Q6MZ06; 20-475.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
KM InterPro; IPR003596; IG_v.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8B CRC64;

Query Match 99.3%; Score 1229; DB 2; Length 475;
Best Local Similarity 99.6%; Pred. No. 2e-91;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKHTCPCPAPBELLGGPSVFLPPPKKDTLMTSRTEVTCVVVDVSHEDPEVKFNMYVD 61
DB 249 DKHTCPCPAPBELLGGPSVFLPPPKKDTLMTSRTEVTCVVVDVSHEDPEVKFNMYVD 308

QY 62 GVEVHNAKTKRREQVSTYRVSVLTVLHODMNGEKYCKVNKAAPAEIKTISKAK 121
DB 309 GVEVHNAKTKRREQVSTYRVSVLTVLHODMNGEKYCKVNKAAPAEIKTISKAK 368

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTIPVLD 181
DB 369 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTIPVLD 428

QY 182 DGSFFLYSKLTVDKSRWQQGNVFCSVMEHGLNHYTQKSLISPGK 228
DB 429 DGSFFLYSKLTVDKSRWQQGNVFCSVMEHGLNHYTQKSLISPGK 475

RESULT 15
Q6N094_HUMAN PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686o01196.
GN Name=DKFZp686o01196;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
NCBI_TaxID=9606;
RX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Esophagus tumor;
RG The German cDNA Consortium;
RA Wambert R., Heubner D., Mewes H.W., Well B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX440622; CAE45776.1; -, mRNA.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KM Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35ABC18 CRC64;

Query Match 99.3%; Score 1229; DB 2; Length 480;
Best Local Similarity 99.6%; Pred. No. 2e-91;
Matches 226; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 DKHTCPCPAPBELLGGPSVFLPPPKKDTLMTSRTEVTCVVVDVSHEDPEVKFNMYVD 61

Db	254	DKHTCPCPAPABELLGGPSVFLPPKPKDITLIMISRTPEVTCVVVDSHEDPEVKENMYVD	313
Qy	62	GVEVHNAKTKREROYNSTYRVSVLTLYLHODMLNGKEYCKVSNKALPAPIEKTISKAK	121
Db	314	GVEVHNAKTKREROYNSTYRVSVLTLYLHODMLNGKEYCKVSNKALPAPIEKTISKAK	373
Qy	122	GQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGOPENNYKTTPVLD	181
Db	374	GQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVWESNNGOPENNYKTTPVLD	433
Qy	182	DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	228
Db	434	DGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK	480

Search completed: March 16, 2006, 20:01:20
 Job time : 231 secs